us-09-698-903b-12.rnpb

```
JS-09-733-151-12
                                                                                                                                                                                                                            December 5, 2004, 06:58:29; Search time 16.704 Seconds (without alignments) 6907.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3694831 segs, 2747406616 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gottggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                          US-09-698-903B-12
21
                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 12, Appl									Sequence 24, Appl		Sequence 2, Appli
ID	9 US-09-733-151-12	US-10-375-332-12	US-09-733-151-39	US-10-375-332-39	US-09-794-384A-7	US-10-801-550-7	US-09-733-151-36	US-10-375-332-36	US-09-733-151-24	US-10-375-332-24	US-10-047-542-13	US-09-733-151-2
DB	6	15	σ	15	σ	17	σv	15	თ	15	13	σ
k Query Match Length DB	21	21	694	694	831	831	606	606	1077	1077	4465	4832
Query Match	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4
Score	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4
Result No.	 H H	7	ю О	Ω	S	9	0	ω U	o O	0 10	11	0 12

RESULT 2 US-10-375-332-12

g

Sequence 2, Appli	Sequence 1, Appli	ਜੇ	۲.	'n	4,	о О	-	_	п,	Sequence 14, Appl	equence 4,	4,	_	(.)	w		•	•		• •	e e	₹.		•	٠.	• •	•	• •	• •	•	•		,
s US-10-375-332-2	US-09-733-151-1	-375	.970-921-	509-945	US-09-509-945-4	US-1(US-1(US-10-047-542	5 US-10-027-880-5	US-10-047-	7	-874-926	US-09-940-550A	US-10-033-19	US-09-792-568-	US-10-250-8	US-10-250-553-	250-	US-10-250-553-2	US-10-250-82	3-10-250-5	3-138	US-10	US-10-407-84	US-09-792-568-	an	e us	US-10-	US-10	US-10-	6 US-10-250-553-25	-811	
832 1	σ	4946 15	•	-	548 9	H	Н	Н	Н	Н	340 9	340 9	٦	7	7	٦	Н	Н	Н	Н	Н	241 9	-	Н	٦	٦	Н	Н	Н	٦		752 1	1
4 4 4	4	92.4	4.	2.4	2.4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4.	4	4	4	4	4		H
4 9 4	4.6	19.4	19.4	19.4	19.4	σ	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4			19.4			19.4		19.4	19.4			6	19.4	0	19.4	10.	F . C T
,) () () ()	 	-	-	18	19	50.	C 21	N	N	N	N	N	10	ומו	N	. (7)	וייז ו	32	ייי	ייי	(7)	90	3.7	•	(*)	, 4	· •	٠,	. 4) C		י יי

ALIGNMENTS

```
ö
                                                                                                                                                  Gaps
                                                                                                                                                  ö
                                                                                                                                     Query Match 92.4%; Score 19.4; DB 9; Length 21; Best Local Similarity 95.2%; Pred. No. 5.7; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                               1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                       GCTTGGACTATAATACCTGAC 21
                                                                                                                                                                 8
```

```
NAMENTEY: misc_feature
NAMENTEY: (1). (694)
UCCATION: (1). (694)
OTHER INFORMATION: sequence comprising the 5' flanking region of RF-BN1 in WOSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09794384A

Sequence 7, Application US/09794384A

Petent No. US20020144305A1

SEQUENCE INFORMATION:
APPLICANT: Dellaporta, Stephen L.
APPLICANT: Moreno, Maria A.

APPLICANT: Moreno, Maria A.

TITLE OF INVENTION: Transmission of a Transgene
TITLE OF INVENTION: Transmission of a Transgene

TITLE OF INVENTION: WINDER: US/09/794,384A

CURRENT APPLICATION NUMBER: US/09/794,384A

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US 60/185,524

PRIOR PILING DATE: 2000-02-28

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Deliaporta, Stephen L.
APPLICANT: Moreno, Maria A.
APPLICANT: Moreno, Maria A.
APPLICANT: Yale University
TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate
TITLE OF INVENTION: Transmission of a Transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.4%; Score 19.4; DB 15; 95.2%; Pred. No. 11;
                              CURRENT APPLICATION NUMBER: US/10/375,332
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US/09/733,151
PRIOR FILING DATE: 2000-12-08
PRIOR PLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 39
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.4%; Score 19.4; Best Local Similarity 95.2%; Pred. No. 11 Matches 20; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        694 GCTTGGACTATAATACCTGAC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664 GCTTGGACTATAATACCTGAC 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10801550 Publication No. US20040154054A1 GENERAL INFORMATION:
          FILE REFERENCE: 514412-2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: polyA signal
; LOCATION: (514)..(813)
US-09-794-384A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-375-332-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-794-384A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-801-550-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)..(694)
OTHER INFORMATION: sequence comprising the 5' flanking region of RF-BN1 in WOSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DE BOCh, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REPERENCE: 514412-2019
CURRENT APPLICATION NUMBER: 105/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
                                                                 APPLICANT: De Both, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REFERENCE: 514412-2019
CURENT APPLICATION WIMBER: US/10/375,332
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US/09/733,151
PRIOR APPLICATION NUMBER: US/09/733,151
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: De Both, et al. TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.4%; Score 19.4; DB 15; Length 21;
illarity 95.2%; Pred. No. 5.7;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
92.4%; Score 19.4; D
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , LOCATION: (1). (21)
; OTHER INFORMATION: primer 201 (BNA01)
US-10-375-332-12
Sequence 12, Application US/10375332
Publication No. US20030188347A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        694 GCTTGGACTATAATACCTGAC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/10375332
Publication No. US20030188347A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCTTGGACTATAATACCTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-733-151-39/c
; Sequence 39, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-375-332-39/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-733-151-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 39
LENGIH: 694
                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 12
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

Gaps

ö

Gaps

```
NUMBER OF SEQ ID NOS: 43

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 36

LENGTH: 909

TYPE: DNA

ORGANISM: Artificail sequence
FRATURE:
NAME/KEY: misc feature
LOCATION: (1)..(909)

LOCATION: (2009)

OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 in WOSR
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
SCANISM: Brassica napus
FRATURE:
NAME/KEY: misc_feature
1.0CATION: (1)...(1077)
OCHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
US-09-733-151-24
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                    Length 909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1077;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.4%; Score 19.4; DB 9;
Best Local Similarity 95.2%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                        Query Match
92.4%; Score 19.4; I
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               980 derredacraraaracerdae 960
                                                                                                                                                                                                                                                                                                                                                    909 GCTTGGACTATAATACCTGAC 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                   1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/09733151

Sequence 36, Application US/09733151

Parent No. US20010029620A1

GENERAL INFORMATION:
APPLICANT: De Both, et al.
TILLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REFRERCE: 514412-2019

CURRENT FILING DATE: 2000-12-08

FRICR APPLICATION NUMBER: 099457,037

PRIOR PRILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin version 3.0

SEQ ID NO 36

LENGTH: 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature; LOCATION: (1)..(909); COCTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 in WOSR US-09-733-151-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  General 36, Application US/10375332
Sequence 36, Application US/10375332
Sequence 36, Application US/10375332
Sequence 36, Application US/10375332
GENERAL INFORMATION:
PUBLICANT: DE BOCH, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REPERENCE: 514412-2019
CURRENT APPLICATION UNMERR: US/10/375,332
CURRENT FILING DATE: 2003-02-7
PRIOR APPLICATION UNMERR: US/09/733,151
PRIOR PLING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 209/457,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                             DB 17; Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
92.4%; Score 19.4; DB 9; Length 909;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                             Query Match 92.4%; Score 19.4; Esst Local Similarity 95.2%; Pred. No. 11; Matches 20; Conservative 0; Mismatches
     FILE REFERENCE: 44574-5078-US
CURRENT APPLICATION NUMBER: US/10/801,550
CURRENT FILING DATE: 2004-03-17
PRIOR APPLICATION NUMBER: US/09/794,384
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 16
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 7
LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  909 GCTTGGACTATAATACCTGAC 889
                                                                                                                                                                                                               TYPE: DNA ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     664 dcircacrararaccidad 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificail sequence
                                                                                                                                                                                                                                                                   ; NAME/KEX: polyA signal
; LOCATION: (514)..(813)
US-10-801-550-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ö

```
PatentIn version 3.0
        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IS-10-375-332-2/c
                                                                     4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-733-151-1/c
                            SOFTWARE:
SEQ ID NO 2
LENGTH: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                           임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09733151

Batent NO. US20010029620A1

GENERAL INFORMATION:
APPLICANT: De Both, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151

CURRENT FILING DATE: 2000-12-08

PRIOR APPLICATION NUMBER: 09/457,037

PRIOR FILING DATE: 1999-12-08
                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LARRICK, JAMES W.
APPLICANT: LARRICK, METH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT PILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-04-28
NUMBER OF SEQ ID NOS: 101
SSOFTWARE: PATENTIN UNIVER: 07/200,298
NUMBER OF SEQ ID NOS: 101
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                     Length 1077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.4%; Score 19.4; DB 13; Length 4465; Best Local Similarity 95.2%; Pred. No. 15; Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Expression-type plasmid pBMSP-1
                                                                                                                                                                   DB 15;
                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                 Query Match 92.4%; Score 19.4; I
Best Local Similarity 95.2%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3659 GCTTGGACTATAATACCTGAC 3679
                                                                                                                                                                                                                                                                                      980 GCTTGGACTATAATACCTGAC 960
                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 13, Application US/10047542; Publication No. US20020168367A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified base
1 LOCATION: (2214)..(2215)
1 OTHER INFORMATION: a, c, t or g
US-10-047-542-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: modified base
LOCATION: (2150)
OTHER INFORMATION: a, c, t
TYPE: DNA
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-10-047-542-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 13
LENGTH: 4465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-733-151-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                           FEATURE:
                                                                                                                                                                                                                                                 ò
```

```
APPLICANT: De Both, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
TITLE REPERENCE: 514412-2019
CURRENT APPLICATION NUMBER: 2009-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: De BOCH, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REPERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/10/375,332
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US/09/733,151
PRIOR PRILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 4832
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4832;
                                                                                                                                                                                                                DB 9; Length 4832;
                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 92.4%; Score 19.4; DB 15; Best Local Similarity 95.2%; Pred. No. 15; Matches 20; Conservative 0; Mismatches 1;
                                                                                                                                                                                                        Query Match
92.4%; Score 19.4; D
Best Local Similarity 95.2%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              163 GCTTGGACTATAATACCTGAC 143
                                                                            ) NAME/KEY: misc_feature

) LOCATION: (1)..(4832)

) CTHER INFORMATION: Plasmid pTHW118

US-09-733-151-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GCTTGGACTATATACCTGAC 143
                                                                                                                                                                                                                                                                                                                1 GCTTGGACTATAATACTTGAC 21

    i NAME/KEY: misc_feature
    i LOCATION: (1)...(4832)
    j OTHER INFORMATION: Plasmid pTHW118
    US-10-375-332-2

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10375332
Publication No. US20030188347A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09733151
Patent No. US20010029620A1
GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
```

us-09-698-903b-12.rnpb

```
Sequence 1, Application US/10375332
; Sequence 1, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
    APPLICANTY DE BOCK, et al.
    TILE REFERENCE: 514412-2019
    CURRENT APPLICATION NUMBER: US/10/375,332
    CURRENT PILING DATE: 2003-02-27
    PRIOR PILICATION NUMBER: US/09/733,151
    PRIOR PLICATION NUMBER: 09/457,037
    PRIOR PLILING DATE: 1999-12-08
    PRIOR PILING DATE: 1999-12-08
    PRIOR PILING DATE: 1999-12-08
    NUMBER OF SEQ ID NOS: 43
    SOFTWARE: Patentin version 3.0
    SEQ ID NO 1
    LENGTH: 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

92.4%; Score 19.4; DB 15; Length 4946;
Best Local Similarity 95.2%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                       Query Match

92.4%; Score 19.4; DB 9; Length 4946;
Best Local Similarity 95.2%; Pred: No. 15;
Matches 20; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                           163 GCTTGGACTATAATACTGAC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
; LOCATION: (1)...(4946)
; OTHER INFORMATION: Plasmid pTHW107
US-10-375-332-1
                      FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(4946)

OTHER INFORMATION: Plasmid pTHW107
US-09-733-151-1
                                                                                                                                                                                                                                                          1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-10-375-332-1/c
                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                             5
C
```

Search completed: December 5, 2004, 09:36:24 Job time : 16.704 secs

163 GCTTGGACTATAATACCTGAC 143

q à

1 GCTTGGACTATAATACTTGAC 21

This Page Blank (uspto)

Н

```
TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                         0 0 0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 10, Appl Sequence 39, Appl Sequence 36, Appl Sequence 36, Appl Sequence 24, Appl Sequence 24, Appl Sequence 2, Appl Sequence 23, Appl S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Appl
Sequence 23, Appl
Sequence 22, Appl
Sequence 2, Appl
Sequence 2, Appli
Sequence 5, Appli
                                                                                                                                                                   December 5, 2004, 05:20:20 ; Search time 3.528 Seconds (without alignments) 4230.886 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents NA:*
1: /cgm2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgm2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgm2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgm2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgm2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgm2_6/ptodata/1/ina/PcTuS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-430-497A-12
US-09-431-12
US-09-431-12
US-09-431-12
US-09-431-131-12
US-09-431-131-39
US-09-733-151-39
US-09-733-151-39
US-09-794-384A-7
US-09-457-037B-36
US-09-457-037B-36
US-09-457-037B-24
US-08-478-015-2
US-08-478-015-2
US-08-478-015-2
US-08-478-015-2
US-09-458-09-2
US-09-458-09-3
US-09-458-09-3
US-09-458-09-3
US-09-458-09-3
US-09-458-09-3
US-09-458-09-3
US-09-458-09-3
US-09-655-782-3
US-09-655-782-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-08-453-104-23
S-08-694-824-23
S-08-694-824-22
S-08-694-824-22
S-09-080-625-2
S-09-695-782-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      824507 segs, 355394441 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 20000000000
                                                                                                                                                                                                                                                                                US-09-698-903B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                900

1111

1110

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1111

1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                   OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
No.
```

υυ

0 0 0 0

```
USE-09-457-037B-12

Sequence 12, Application US/09457037B

Sequence 12, Application US/09457037B

Parent No. 650663

GENERAL INFORMATION:

APPLICANT: De Both, et al.

TITE OF INVENTION: HYBERD WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
FILE REFERENCE: 514412-2019

CURRENT APPLICATION NUMBER: US/09/457,037B

CURRENT APPLICATION NUMBER: 09/457,037

PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.0

SEQ ID NO 12

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
FEATURE:

FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-430-497A-12
US-09-430-497A-12
US-09-430-497A-12

Sequence 12, Application US/09430497A

Sequence 12, Deplication US/09430497A

Sequence 12, Deplication US/09430497A

JEGNERAL INFORMATION:
APPLICANT: DE BEUCKELEER, Marc

APPLICANT: DE BEUCKELEER, Marc

TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING

TITLE OF INVENTION: SAME

TITLE OF INVENTION: SAME

TITLE OF INVENTION: UNDER: US/09/430,497A

CURRENT FILING DAME: 1999-10-29

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                       Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                       Sequence Seq
                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ), OTHER INFORMATION: Description of Artificial Sequence: MDB201
US-09-430-497A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 21; Conservative 0; Mismatches 0; Indels
US-09-695-782-5
US-09-680-625-4
US-09-457-732-4
US-09-733-151-2
US-09-733-151-2
US-09-733-151-1
US-09-458-093-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4444444444444444
```

Ŋ

ö

```
. LOCATION: (1) [(694)
. OTHER INFORMATION: sequence comprising the 5' flanking region of RF-BN1 in WOSR
US-03-457-037B-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-457-037B-39/c

Sequence 39, Application US/09457037B

Facent No. 5560563

GRENAL INFORMATION: 
APPLICANT: DE BOth, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/457,037B

CURRENT APPLICATION NUMBER: 09/457,037

FRICK APPLICANTON TELLAY
NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.0

SEQ ID NO 39

LENGTH: 694
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WESTON, Brigitte
APPLICANT: WESTON, Brigitte
APPLICANT: DE BEUCKELEER, Marc
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: SAME
FILE REFERENCE: 514412-2020
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT PILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
GRGANISM: Artificial Sequence
FEATURE:
GOTHER INFORMATION: Description of Artificial Sequence: 3' border
GOTHER INFORMATION: flanking region of elite event MS-B2
NAME/KET: misc feature
COTHER INFORMATION: 1-103)
GOTHER INFORMATION: T-DNA
NAME/KET: misc feature
LOCATION: (1947...(195)
GOTHER INFORMATION: plant DNA
US-09-430-497A-10
                                                                                                                                       ..
0
                                                                                 Query Match 92.4%; Score 19.4; DB 4; Length 415; Best Local Similarity 95.2%; Pred. No. 0.9; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.4%; Score 19.4; DB 4; Length 416; 95.2%; Pred. No. 0.9; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09430497A Patent No. 6509516
                                                                                                                                                                                                                                     335 GCTTGGACTATAATACCTGAC 315
                                                                                                                                                                                       1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 GCTTGGACTATAATACCTGAC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.2%
Matches 20; Conservative
  ; OTHER INFORMATION: T-DNA US-09-430-497A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                    -09-430-497A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Pat
SEQ ID NO 10
LENGTH: 416
                                                                                                                                                                                       8
                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: De Both, et al.
APPLICANT: De Both, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REFERENCE: 5.14412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SSOFTWARE: Patentin version 3.0
LENGTH: 21
                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: WESTON, Brigitte
APPLICANT: DE BEUCKELEER, Marc
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: SAME
FILE REFERENCE: 514412-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
SEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 5' border
OTHER INFORMATION: flanking region of elite event MS-B2
NAME/KEY: misc feature
LOCATION: (1).7(234)
OTHER INFORMATION: plant DNA
NAME/KEY: misc feature
LOCATION: (235)..(415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                         Ouery Match 92.4%; Score 19.4; DB 4; Length 21; Best Local Similarity 95.2%; Pred. No. 0.66; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.4%; Score 19.4; DB 4; Length 21; Best Local Similarity 95.2%; Pred. No. 0.66; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
FEG. ID NO 8
          LUCCATION: (1). (21)
COTHER INFORMATION: primer 201(BNA01)
US-09-457-037B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) LOCATION: (1). 7(21)
; OTHER INFORMATION: primer 201(BNA01)
US-09-733-151-12
                                                                                                                                                                                                                                  1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                1 ścirgsaciararaccigac 21
                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-733-151-12
Sequence 12, Application US/09733151
Patent No. 6563026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09430497A Patent No. 6509516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ścirgsacraratraccreac 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-430-497A-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db
```

8

```
RESULT 9
US-09-457-037B-36/C
; Sequence 36, Application US/09457037B
; Sequence 36, Application US/09457037B
; Patent No. 6506963
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US/09/457,037
; PRIOR PILING DATE: 1999-12-08
; SOFTWARE: Patentin version 3.0
; SOFTWARE: Patentin version 3.0
; LENGTH: 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(909)
CTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 in WOSR
US-09-733-151-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35, Application US/09733151

Sequence 35, Application US/09733151

Patent No. 6563026

PREMEMATION:
APPLICANT: DE Both, et al.
TITLE OF INVENTION:
FILE REFERENCE: 514412-2019

CURRENT FILING DATE: 2000-12-08

CURRENT FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTING DATE: PATENTING DATE: PATENTING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 36

LINGTH: 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA

SOGANISM: Artificial sequence

PEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(909)

SOTHER INFORMATION: sequence comprising the 5' flanking region of MS-BNI in WOSR

US-09-457-037B-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
92.4%; Score 19.4; DB 4; Length 909;
Best Local Similarity 95.2%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
92.4%; Score 19.4; DB 4; Length 909;
Best Local Similarity 95.2%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             909 GCTTGGACTATAATACCTGAC 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                909 dcirdaacraraaraccraac 889
                                                              664 GCTTGGACTATAATACCTGAC 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCTTGGACTATAATACTTGAC 21
21
1 GCTTGGACTATAATACTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificail sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-457-037B-24/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
LOCATION: (1). (694)
COTHER INFORMATION: sequence comprising the 5' flanking region of RF-EN1 in WOSR
US-09-733-151-39
                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-733-151-39/C
US-09-733-151-39/C
Sequence 39, Application US/09733151
Sequence 39, Application US/09733151
Sequence 39, Application US/09733151
Sequence 39, Application US/0973351
Sequence 39, Application US/097335151
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION UNMERR:
TOTREENT APPLICATION NUMBER:
CURRENT APPLICATION NUMBER:
TOTREENT APPLICATION NUMBER:
SOFTRAFE:
PRIOR PAPPLICATION NUMBER:
PRIOR PRIOR FILING DATE:
PRIOR PRIOR FILING DATE:
SOFTWARE:
SOFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8

US-09-794-384A-7

is Sequence 7, Application US/09794384A

j Sequence 7, Application US/09794384A

j Patent No. 6743968

j GENERAL INFORMATION:
 j APPLICANT: Dellaporta, Stephen L.
 j APPLICANT: Moreno, Maria A.
 j APPLICANT: Wareno, Maria A.
 j APPLICANT: Yale University
 j TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate
 j TITLE OF INVENTION: Transmission of a Transgene
 j FILE REFERENCE: 44574-5078-US
 j CURRENT AILING DATE: 2001-02-28
 j PRIOR FILING DATE: 2000-02-28
 j NUMBERS OF SEQ ID NOS: 16
 j SEQ ID NO 7
 j LENGTH: 831
 j LENGTH: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
92.4%; Score 19.4; DB 4; Length 831;
Best Local Similarity 95.2%; Pred. No. 0.96;
Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
92.4%; Score 19.4; DB 4; Length 694;
Best Local Similarity 95.2%; Pred. No. 0.94;
Matches 20; Conservative 0; Mismatches 1; Indels (
                                 Query Match

92.4%; Score 19.4; DB 4; Length 694;
Best Local Similarity 95.2%; Pred. No. 0.94;
Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  694 GCTTGGACTATAATACTGAC 674
                                                                                                                                                                                                                              694 GCTTGGACTATAATACCTGAC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                 1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: polyA signal
; LOCATION: (514)..(813)
US-09-794-384A-7
                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
NAME/KEY: - 791..1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: -
LOCATION: 1.8
OTHER INFORMATION: /
OTHER INFORMATION: t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: - . . 790
LOCATION: 9..790
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DN HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            % Sequence 24, Application US/09733151

§ Sequence 24, Application US/09733151

§ Patent No. 6563026

§ GENERAL INFORMATION:

§ TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME

§ FILE REPERENCE: 514412-2019

§ CURRENT APPLICATION NUMBER: US/09/733,151

§ CURRENT FILING DATE: 2000-12-08

§ FRICK APPLICATION NUMBER: 09/457,037

§ PRICK PILING DATE: 1999-12-08
Sequence 24, Application US/09457037B
Patent No. 6506963
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTYON: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REPRENCES: 514412-2019
CURRENT APPLICATION NUMBER: US/09/457,037B
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTION DATE: 1999-12-08
SOFTWARE: PATENTION OF 14
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature;
10CATION: (1)._(1077)
10THER INFORMATION: sequence comprising the 5' flanking region of RF-BN1
NAME/KEY: misc feature
1 LOCATION: (1)._(45)
1 OTHER INFORMATION: pGEM-T vector
US-09-457-037B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) LOCATION: (1). [(1077) ) CTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 US-09-733-151-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.4%; Score 19.4; DB 4; Length 1077; Best Local Similarity 95.2%; Pred. No. 0.99; Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 1077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.4%; Score 19.4; DB Best Local Similarity 95.2%; Pred. No. 0.99; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        980 GCTTGGACTATAATACCTGAC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   980 GCTTGGACTATAATACCTGAC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-064-121-2
                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
```

```
TITLE OF INVENTION: ROCCESS FOR TANISPORNING
TITLE OF INVENTION: KONCOTATED TANIS

OKNESS OF SEQUENCES: 5

CORRESPONDED FOR SECUENCES OF A Maching TO Receive & Maching To Receiv
```

. 0

> Sequence 2, Application US/08064121 Patent No. 5641664 GENERAL INFORMATION: APPLICANT: D'HALLUIN, Kathleen

ö

Gaps ö

1; Indels

0; Mismatches

```
/note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                         PERTEAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O'BEL, Blke
TITLE OF INVENTION:
MONOCOTYLEDONOUS PLANTS
NUTHER OF INVENTION:
MONOCOTYLEDONOUS PLANTS
TITLE OF INVENTION:
MONOCOTYLEDONOUS PLANTS
NUTHER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSE:
ADDRESS:
ADDRESSE:
ADDRESS:
ADDRESSE:
AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                        1113 GCTTGGACTATAATACCTGAC 1133
                                      1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                               US-08-475-975-2
; Sequence 2, Application US/08475975
; Patent No. 6002070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
FRATURE:
NAME/KEY: -
LOCATION: 1.8
COCATION: 1.9
OTHER INFORMATION: V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: 9..790
LOCATION: 9..790
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAMPIKEY:
NAMPIKEY:
NAMPIKEY:
OTHER INFORMATION: /label= 3'g7
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation
OTHER INFORMATION: site derived from Agrobacterium T-DNA gene 7"
US-08-478-015-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= NPTII
/note= "coding sequence of neomycine phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "sequence derived from
tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19.4; DB 1; Length 1186; Pred. No. 1;
                                                                                                                                                                                                                                                                             RESULT 14
US-08-478-015-2
Sequence 2, Application US/08478015
Sequence 2, Application US/08478015
Sequence 2, Application US/08478015
Sequence 2, Application US/08478015
Sequence 3, Application US/08478015
Septicant Normanian Normanian Applicant Gober, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCE: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.4%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION: 1..8
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY:
LOCATION: 9..790
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
```

us-09-698-903b-12.rni

```
0;
) OTHER INFORMATION: /label= 3/g7 OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium US-08-475-975-2
                                                                                                                                                                           0; Gaps
                                                                                                                              Query Match 92.4%; Score 19.4; DB 3; Length 1186; Best Local Similarity 95.2%; Pred. No. 1; Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                               ò
```

Search completed: December 5, 2004, 07:17:54 Job time : 4.528 secs

Ор

Sequence 3, Appli Sequence 3, Appli Sequence 144465, Sequence 144465, Sequence 28593, A Sequence 28593, A Sequence 27021, A Sequence 27021, A Sequence 352, Appl Sequence 261251, Sequence 261251,

5 US-01-759-359A-3 10 US-02-759-359A-3 10 US-09-918-955-3102 3 US-09-918-955-3102 3 US-09-918-955-3102 3 US-10-027-632-144465 5 US-10-036-493-14465 5 US-10-036-493-1466 10 US-10-432-115-2559 10 US-10-437-963-27021 10 US-09-939-825-4 4 US-10-108-846-12468 4 US-10-108-846-12468 5 US-10-037-270-352 10 US-10-037-478-10553 10 US-10-027-632-261250 10 US-10-027-632-261250 10 US-10-037-478-10553 10 US-10-027-478-10553 10 US-10-021-323-7468 10 US-10-437-963-79931

Sequence 3470, Ap

```
1 GAAATCCATGTAAAGCAGCAGGG 23
1728
1728
90541
90541
90541
468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-923-876-5059/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5059, Ap
Sequence 2059, Ap
Sequence 239504,
Sequence 239505,
Sequence 239505,
Sequence 23, Appli
Sequence 11151, A
Sequence 143567,
Sequence 143567,
Sequence 97618, A
Sequence 97619, A
                                                                                                                                       2004, 06:58:29 ; Search time 18.2949 Seconds (without alignments) 6907.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*

| cgn2_6/ptodate12/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/PCT_RMEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/DS06_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US106_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/US106_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/US106_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/US10C_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/US10C_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/US10C_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodate2/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodate3/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodate3/pubpna/US10_NEW_PUB.seq:*
| cgn2_6/ptodate3/pubpna/US10_NEW_PUB.seq:*
| cgn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seg:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 US-09-923-876-5059

3 US-10-027-632-239504

3 US-10-027-632-239505

5 US-10-027-632-239505

6 US-10-027-632-239505

6 US-10-275-287-2

10S-09-864-761-11151

3 US-10-027-632-143567

5 US-10-027-632-143567

3 US-10-027-632-143567

3 US-10-027-632-97618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-923-876-5059
                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                           3694831 segs, 2747406616 residues
                                                                                                                                                                                                                                                            gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      nucleic search, using sw model
                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
                                                                                                                                                                                                                US-09-698-903B-11
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
572
572
572
572
672
478
628
628
1728
                                                                                                                                           'n
                                                                                                                                             December
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.7
80.0
80.0
80.0
80.0
79.1
75.7
75.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                      OM nucleic -
                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126460111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00000000
```

```
RESULT 1
US-09-23-876-5059/c
US-09-223-876-5059/c
US-09-223-876-5059/c
US-09-223-876-5059/c
US-09-223-876-5059/c
US-09-223-876-5059/c
US-09-223-876-5059/c
US-09-223-876-505013598A1
GENERAL INFORMATION: Badhurath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: AND ENGINE DEADLY CONTINES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
TITLE OF INVERTION: POLYMUCIECOILES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT APPLICATION NUMBER: 00/98-9.32
PRIOR APPLICATION NUMBER: 00/085,331
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-06-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
LENGTH: 173
TENGTH: 174
TENGTH: 174
TENGTH: 175
T
```

```
US-10-027-632-239504/c
        ; ORGANISM: Human
US-10-027-632-239504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-027-632-239505
                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                    Sequence 5059, Application US/09923876

Publication No. US20030237110A9

GENERAL INCORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Aserman, Bradley K.
TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: 05/09/923,876

CURRENT APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR PLILNG DATE: 1999-04-21
PRIOR PLILNG DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGram
SEQ ID NOS: 6332
SOFTWARE: PERL PROGram
SEQ ID NOS: 6332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | JAPLICANT: MATGY, David G. |
| JAPLICANT: Wargy, David G. |
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| FILE REFERENCE: 10827.129 |
| CURRENT APPLICATION NUMBER: US 60/218,006 |
| PRIOR FILING DATE: 2000-01-20 |
| PRIOR FILING DATE: 2000-04-20 |
| PRIOR FILING DATE: 2000-04-20 |
| PRIOR FILING DATE: 2000-04-20 |
| PRIOR FILING DATE: 2000-04-24 |
| PRIOR FILING DATE: 2000-02-4 |
| PRIOR FILING DATE: 2000-02-4 |
| PRIOR PELICATION NUMBER: US 60/165,368 |
| PRIOR APPLICATION NUMBER: US 60/165,368 |
| PRIOR APPLICATION NUMBER: US 60/166,358 |
| PRIOR PILING DATE: 1999-09-28 |
| PRIOR FILING DATE: 1999-09-28 |
| PRIOR FILING DATE: 1999-08-08 |
| PRIOR FILING DATE: 1999-08 |
| PRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030237110A9 700456286H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.7%; Score 18.8; D
87.0%; Pred. No. 63;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure

LOCATION: 58, 115, 143

COTHER INFORMATION: a, t, c, g, or other

US-09-923-876-5059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 239504, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
129 GACATCCATGTAACNCAGCAGGG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 dacarccardraacncadcaddd 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.0°
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-027-632-239504/c
                                                                                                                                                             RESULT 2
US-09-923-876-5059/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 239504
LENGTH: 572
TYPE: DNA
                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                     Sequence 239565. Application US/10027632

Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION UNMBER: US/0.202-04-30
PRIOR APPLICATION NUMBER: US/0.202-04-30
PRIOR APPLICATION NUMBER: US/0.198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 1000-03-24
PRIOR PILING DATE: 1099-11-23
PRIOR APPLICATION NUMBER: US/0.165,368
PRIOR PILING DATE: 1099-08-09-36
PRIOR PILING DATE: 1099-08-09-36
PRIOR PILING DATE: 1099-08-09
PRIOR PILING DATE: 1099-08-09
PRIOR PILING DATE: 1399-08-09
PRIOR PILING DATE: 1399-08-08-09
PRIOR PILING DATE: 1399-08-08-08
PRIOR PILING DATE: 1399-08-08-08
PRIOR PILING DATE: PASEED FOR WINDOWN Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: World, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 10882 7.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR RILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
      Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 572;
                                                                  Indels
Score 18.4; DB 13;
Pred. No. 1.2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%; Score 18.4; DB 13;
95.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 239504, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                               369 AAAGCCATGTAAAGCAGCAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 AAAGCCATGTAAAGCAGCAG 350
                                                                                                                                    2 AAATCCATGTAAAGCAGCAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AAATCCATGTAAAGCAGCAG 21
Query Match
Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.03
Matches 19; Conservative
```

```
Sequence 11151, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: GENORE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 16570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               °
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 18.4; DB 1
95.0%; Pred. No. 2e+02;
tive 0; Mismatches
                                PRIOR APPLICATION UNMBER: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/EPO2/01867
PRIOR FILING DATE: 2002-02-21/PC02/01867
PRIOR PELING DATE: 2002-02-21/PC044.7
PRIOR PELING DATE: 2001-07-02
PRIOR PILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 58
SOCIETA PACENTIN NOS: 58
SEQ ID NO SEQ ID NOS: 58
LENGTH: 16570
LENGTH: 16570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 2923-212
CURRENT APPLICATION NUMBER: US/10/275,287
CURRENT FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US01/00662 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12888 GAAGTCCATGTAAAGCAGCA 12869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAATCCATGTAAAGCAGCA 20
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CRGANISM: Human cytomegalovirus
US-10-275-287-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-864-761-11151/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10275287
Publication No. US20040087001A1
GENERAL INFORMATION:
TITLE OF INVENTION: Recombinant vector containing infectious human cytomegalovirus ge
TITLE OF INVENTION: with preserved wild-type characteristics of clinical isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FULLICALLIA NO. LOZZOUJUZUERO JASA

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,483
PRIOR FILING DATE: 2000-03-29
PRIOR PRIDE APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-38
PRIOR PRIOR FILING DATE: 1999-08-38
PRIOR FILING DATE: 1999-08-38
PRIOR FILING DATE: 1999-08-38
PRIOR PRIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.4; DB 15; Length 572;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.4; DB 15;
Pred. No. 1.2e+02;
PRIOR APPLICATION NUMBER: US CV, T. PRIOR FILING DATE: 1999-11-23 PRIOR FILING DATE: 1999-11-23 PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-08-09 PRIOR FILING DATE: 1999-08-09 PRIOR FILING DATE: 1999-08-09 PRIOR FILING DATE: 1999-08-09 PRIOR FILING SAFE OF UNIMBER OF SOF ID NOS: 325720 SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 239504 LENGTH: 572
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 80.0%; Score 18.4; D
Best Local Similarity 95.0%; Pred. No. 1.2e
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 239505, Application US/10027632
Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 AAAGCCATGTAAAGCAGCAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 AAAGCCATGTAAAGCAGCAG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AAATCCATGTAAAGCAGCAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AAATCCATGTAAAGCAGCAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -10-027-632-239505/c
                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-239504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Human
US-10-027-632-239505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-275-287-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

g à

```
US-10-027-632-97618/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-143567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 143667; Application US/10027632

Publication No. US2020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108877.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR PELICATION NUMBER: US 60/199,006

PRIOR PELING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1000-03-29

PRIOR FILING DATE: 1000-03-29

PRIOR FILING DATE: 1099-11-23

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-09-28

PRIOR PELING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720

SOFTWARE FEASTSEE FEASTSEE FEASTSEE FEASTSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.7%; Score 17.4; DB 13; Length 628; 94.7%; Pred. No. 3.6e+02; ive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.1%; Score 18.2; DB 9; Length 478; Best Local Similarity 87.0%; Pred. No. 1.4e+02; Matches 20; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                          FEATURE:

OTHER INFORMATION: MAP TO AC005083.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.48

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.43

OTHER INFORMATION: EXPRESSED IN BOUR MARROW, SIGNAL = 0.43

US-09-864-761-11151
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION WUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTHARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11151
LENGTH: A178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 143567, Application US/10027632; Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 GACATCCATGTAAGGAAGCAGGG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAAAICCAIGIAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ATCCATGTAAAGCAGCAGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-143567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-10-027-632-143567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
```

```
WENTER OF INVESTION: Identification and Mapping of Single Nucleotide
FILE OF INVESTION: Identification and Mapping of Single Nucleotide
FILE OF INVESTION: Identification and Mapping of Single Nucleotide
FILE OF INVESTION: Identification and Mapping of Single Nucleotide
FILE OF INVESTION: 100827.139
CURRENT FILEND ADER: 1000-01-20 (1-20)
FRICK FILEND ADER: 1000-01-20 (1-20)
FRICK
```

```
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 97618
LENGTH: 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-10-027-632-97619/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Human
US-10-027-632-97619
                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-97618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-759-359A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
            ô,
                                                                                                                                                                                                                                                               us-lu-uz/-612/4/bly/c
sequence 97619, Application US/10027632
publication No. US2002019331A1
rITLE OF INVENTION: Identification and Mapping of Single Nucleotide
rITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/219,06
PRIOR FILING DATE: 2000-00-12
PRIOR PELING DATE: 2000-00-12
PRIOR PELING DATE: 2000-00-12
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-10-23
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-06-28
PRIOR PRING DATE: 1999-06-09
PRIOR PLING DATE: 1999-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-10.7532-9312-97189/C
Sequence 97618, Application US/10027632
Publication No. US20030204075A9
SERREL INFORMATION:
APPLICANT. Wang, David G
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE PREFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1000-03-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1099-11-23
PRIOR PILING DATE: 1099-11-23
PRIOR PILING DATE: 1099-18-8
PRIOR PILING DATE: 1999-18-8
PRIOR PILING DATE: 1999-18-8
PRIOR PILING DATE: 1999-18-8
PRIOR PILING DATE: 1999-02-8
            Gaps
                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.4; DB 13;
Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
75.7%; Score 17.4; D
Best Local Similarity 94.7%; Pred. No. 4.2e
Matches 18; Conservative 0; Mismatches
                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1710 gaaarccargraaagcacc 1692
                                                                                                                                    1710 GAAATCCATGTAAAGCACC 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAAATCCATGTAAAGCAGC 19
                                                                          1 GAAATCCATGTAAAGCAGC 19
                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-10-027-632-97618/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Human
US-10-027-632-97619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM:
                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                       쉱
```

```
Sequence 3, Application US/09759359A
Sequence 3, Application US/09759359A
Sequence 3, Application US/09759359A
Sequence 3, Application US/09759359A
Sequence 3, Application US/080410NI
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001043
CURRENT APPLICATION NUMBER: US/09/759,359A
CURRENT APPLICATION NUMBER: US/09/759,359A
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                US-IU-UZ/-6249/14/0

Sequence 97619, Application US/10027632

Publication No. US2003020407549

Publication No. US2003020407549

Publication No. US2003020407549

APPLICANT: Wang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome

FITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108627.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR PLING DATE: 2000-07-24

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-108-09

PRIOR PLING DATE: 1999-108-09

PRIOR PLING DATE: 1999-108-09

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1728;
75.7%; Score 17.4; DB 15; Length 1728; 94.7%; Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.7%; Score 17.4; DB 15; Best Local Similarity 94.7%; Pred. No. 4.2e+02; Matches 18; Conservative 0; Mismatches 1;
                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1710 dalatricardraladecace 1692
                                                                                                                                                                                                            1710 GAAATCCATGTAAAGCACC 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAAATCCATGTAAAGCAGC 19
                                                                                                                                                        1 GAAATCCATGTAAAGCAGC 19
        Query Match
Best Local Similarity 94.7
Matches 18; Conservative
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-09-759-359A-3

Query Match
Best Local Similarity 94.7%; Score 17.4; DB 9; Length 90541;
Best Local Similarity 94.7%; Pred. No. 7.96+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AATCCATGTAAAGCAGCAG 21

Db 66140 AATCCATGTAAAGCAGCAG 66158

Search completed: December 5, 2004, 09:36:24
Job time: 20.2949 secs
```

us-09-698-903b-11.rni

```
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Appl
Sequence 8, Appli
Sequence 10, Appli
Sequence 3, Appli
Sequence 13425, Appli
Sequence 13425, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 15579, Appli
Sequence 2051, Appli
Sequence 2051, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 26, Appli
Sequence 27, Appli
                                                                                                                                                                                                               December 5, 2004, 05:20:20; Search time 3.864 Seconds (without alignments) 4230.886 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lssued_Patents NA:*
1: /cgn2 6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2 6/ptodata/1/ina/AB_COMB.seq:*
5: /cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
6: /cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-430-497A-11
US-09-430-497A-8
US-09-430-497A-8
US-09-759-359A-10
US-09-759-359A-10
US-09-759-359A-3
US-09-270-973-3
US-09-270-372-3
US-09-621-976-118
US-09-727-655B-8
US-09-727-655B-8
US-09-727-655B-8
US-09-728-303-7
US-09-749-692-1
US-09-749-692-1
US-09-946-239-7
US-09-946-239-7
US-09-946-239-7
US-09-946-239-7
US-09-946-239-7
US-09-919-039-293
US-09-919-039-293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                824507 segs, 355394441 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                     1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                              - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                   US-09-698-903B-11
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \begin{array}{c} \mathbf{1} \\ \mathbf{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                              OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
                                                                                                                                                                                                                         Run on:
```

Sequence 9, Appli Sequence 26, Appl Sequence 25, Appl Sequence 25, Appl Sequence 2885, Appl Sequence 2, Appl Sequence 2, Appl Sequence 1, Appli Sequence 1, Appli Sequence 11, Appli Sequence 183, App Sequence 183, Appl Sequence 185, Appl Sequence 185, Appl Sequence 185, Appl Sequence 185, Appl Sequence 185, Appl Sequence 185, Appl	метн	Length 23; Indels 0; Gaps 0;	AND METHOD FOR PRODUCING
28 16.2 70.4 27 3 US-09-372-498-9 C 29 16.2 70.4 499 4 US-09-513-999C-260 C 31 16.2 70.4 717 2 US-08-702-25 C 32 16.2 70.4 717 2 US-08-702-25 C 33 16.2 70.4 717 4 US-09-218-471-25 C 34 16.2 70.4 1221 4 US-09-248-471-2 C 35 16.2 70.4 1417 4 US-09-268-097A-1 C 36 16.2 70.4 1417 4 US-09-68-097A-1 C 36 16.2 70.4 1613 2 US-08-899-371-2 C 39 16.2 70.4 1613 2 US-08-899-371-2 C 40 16.2 70.4 2060 4 US-09-825-294-183 C 41 16.2 70.4 2060 4 US-09-825-294-183 C 42 16.2 70.4 2060 4 US-09-713-183 C 43 16.2 70.4 2060 4 US-09-713-550-183 C 44 16.2 70.4 2060 4 US-09-713-550-185 C 45 16.2 70.4 2060 4 US-09-713-50-185	ALIGNMENTS (09430497A i.e. Marc. STERILE BRASSICA PLANTS (10-29) 11 11 21 21 22 32 34 30 30 30 30 30 30 30 30 30	Ouery Match Best Local Similarity 100.0%; Pred. No. 0.04; Matches 23; Conservative 0; Mismatches 0; Qy GAAATCCATGTAAAGCAGGAGG 23 Db GAAATCCATGTAAAGCAGGAGG 23	RESULT 2 US-09-430-497A-8 Sequence 8, Application US/09430497A Sequence 8, Application US/09430497A Patcent No. 6509516 GENERAL INFORMATION: APPLICANT: WESTON, Brigitte APPLICANT: DE BEUCKELEER, Marc TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS); TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS); CURRENT APPLICATION NUMBER: US/09/430,497A CURRENT FILING DATE: 1999-10-29 NUMBER OF SEQ ID NOS: 14 SOFTWARE: PatentIN Ver. 2.1 SOFTWARE: PatentIN Ver. 2.1 SOFTWARE: DAA CURRENT STERICE STERILE BRASSICA PLANTS); NUMBER OF SEQ ID NOS: 14 SOFTWARE: PatentIN Ver. 2.1 SOFTWARE: PatentIN Ver. 2.1 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE STERILE BRASSICA PLANTS); PURBER OF SEQ ID NOS: 14 SOFTWARE: PATENTE STERILE STER

```
) Sequence 352, Application US/09620312D ; Patent No. 6569662
                                                                                                                                                                                         3 AATCCATGTAAAGCAGCAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AATCCATGTAAAGCAGCAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AAATCCATGTAAAGCAGCAGGG
                                                                                            Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 94.7
Matches 18, Conservative
                              ORGANISM: Human
US-09-759-359A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-09-620-312D-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 90541
                                                                                                                                                                                                                                                                                                   RESULT 5
US-10-207-973-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-207-973-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ABU-THREIDEH, Jane et al
TITLE OF INVENTION:
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOO1043
CURRENT FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3:
LENGTH: 90541
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-430-497A-10/C
Sequence 10, Application US/09430497A
Sequence 10, Application US/09430497A
Patent No. 6509516
GENERAL INFORMATION:
APPLICANT: WESTON, Brigitte
APPLICANT: WESTON, Brigitte
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: SAME
FILE REFRENCE: 514412-205
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                               Query Match 100.0%; Score 23; DB 4; Length 415; Best Local Similarity 100.0%; Pred. No. 0.077; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 4; Length 416; 100.0%; Pred. No. 0.077; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: 5
OTHER INFORMATION: flanking region of elite event MS-B2
NAME/KEY: miso feature
1.0CATION: (13. Ceature
OTHER INFORMATION: plant DNA
NAME/KEY: miso feature
1.0CATION: (235)...(415)
1.0CATION: (235)...(415)
1.0CATION: (235)...(415)
1.0CATION: 0.0THER INFORMATION: T-DNA
US-09-430-497A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: flanking region of elite event MS-B2
NAME/KBY: misc feature
LOCATION: (1). (193)
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                               152 GAAATCCATGTAAAGCAGCAGGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 GAAATCCAIGTAAAGCAGCAGGG 241
                                                                                                                                                                                                                                                                                                                      1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/09759359A; Patent No. 6492153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (194)...(416)
OTHER INFORMATION: plant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-430-497A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-09-759-359A-3
                                                                                                                                                                                                                                                                                                                                                            ΩD
                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICAMY: ABD'THREIDEH, Jane et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOO1043

CURRENT FILING DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0
                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-09-270-767-13425/c

"Sequence 13425, Application US/09270767

"Sequence 13425, Application US/09270767

"GENERAL INFORMATION:

"APPLICANT: Homburger et al.

"TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

"TITLE OF INVENTION: Nucleic 326-094

"CURRENT APPLICATION NUMBER: US/09/270,767

"NUMBER OF SEQ ID NOS: 62517

"SEQ ID NO 13425

"ENGTH: 1909
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
Length 90541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.7%; Score 17.4; DB 4; Length 90541; 94.7%; Pred. No. 1.2e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 1909;
                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
Score 17.4; DB 4;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.2; DB
Pred. No. 65;
0; Mismatches
                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 AAATTCATCTCAAGCAGCAGGG 272
                                                                                                                                     66140 AATCCATGTAAAGGAGCAG 66158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66140 AATCCATGTAAAGGAGCAG 66158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                           ; Sequence 3, Application US/10207973 ; Patent No. 6753175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13425
```

```
APPLICATION NUMBER: US/08/894,344C
FILING DATE: 15-AUGUST-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP343700/95
FILING DATE: 28-DECEMBER-1995
FILING DATE: 27-DECEMBER-1996
ATTORNEY/AGENT INFORMATION:
NAME: PERTY, LAWIENCE S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPRAX: 212-218-2100
TELEFAX: 212-218-2200
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CARRACTERISTICS:
LENGTH: 8874 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE: ORGANISM: SACCHAROMYCES CETEVISIAE
STRANDEDNESS: SACCHAROMYCES CETEVISIAE
STRANDEN: SACCHAROMYCES CETEVISIAE
STRANDEN: SACCHAROMYCES CETEVISIAE
STRANDEN: SACCHAROMYCES CETEVISIAE
STRANDEN: SACCHAROMYCES
STRAIN: X2180-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08894344C
; Sequence 1, Application US/08894344C
; Patent No. 6,172196
; GENERAL INFORMATION:
APPLICANT: KANGAL, Masaya
APPLICANT: TOKAL, Masaya
APPLICANT: WINCHI, Yasuhiro
TITLE OF INVENTION: DAN ENCODING PROTEIN COMPLEMENTING
TITLE OF INVENTION: LOW TEMPERATURE-SENSITIVE FERMENTABILITY
ITLE OF INVENTION: LOW TEMPERATURE-SENSITIVE FERMENTABILITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEB: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 30 Rockefeller Plaza
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 10.112-381E FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1440 KD storage.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1440 KD storage.
COMPUTER: IBM PS/V
COMPUTER: LEADABLE FORM:
SOFTWARE: PATENT AID Verl.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 4495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Drmanac, Radoje T.
TITLE OP INVENTION: No. 656966221 Nucleic Acids and
TITLE OP INVENTION: Polypeptides
TITLE OP INVENTION: Polypeptides
FILE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312B
CURRENT PILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR RILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_Teenes Version 1.0
SEQ ID NO 352 L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٠,
ښ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.8%; Score 17.2; Dest Local Similarity 86.4%; Pred. No. 79; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3034 AACTCCTTGTAAAGCAGCAGAG 3055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AAATCCATGTAAAGCAGCAGGG 23
                                                 Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Felyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Mang, Jian-Rui
Zhou, Ping
Ma, Yunging
Ma, Yunging
Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (307)..(3006)
US-09-620-312D-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-894-344C-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-125-028-1/C
US-09-125-028-1/C
Sequence 1, Application US/09125028A
; Patent No. 6190707
; GENERAL INFORMATION:
    APPLICANT: OALAVIZZA, Didier
    APPLICANT: COLAVIZZA, Annie
    FILE REFERENCE: Levure sensible froid
    CURRENT FILING DATE: 1998-08-07
    CURRENT FILING DATE: 1997-02-07
    NUMBER OF SEQ ID NOS: 2
    SOFFWARE: Patentin Ver. 2.1
    SEQ ID NO 1
    LENTH: SE21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
74.8%; Score 17.2; DB 3; Length 8874;
Best Local Similarity 86.4%; Pred. No. 92;
Matches 19; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7552 AAATTAATGTAAAGCACCAGGG 7531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AAATCCATGTAAAGCAGCAGGG 23
                                                                                                 FEATURE:
NAME/KEY: cleavage-site
LOCATION: 1291 to 1296
IDENTIFICATION METHOD: S
                                                                                                                                                                                                                                                                                                        NAME/KEY: cleavage-site
LOCATION: 5927 to 5032
IDENTIFICATION METHOD: S
                                                                                                                                                                                                                                         LOCATION: 4388 to 4393
IDENTIFICATION METHOD: S
                                                                                                                                                                                       FEATURE:
NAME/KEY: cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: cleavage-site
LOCATION: 7675 to 7680
IDENTIFICATION METHOD: 8
                                                      LOCATION: 1 to 8874 IDENTIFICATION METHOD:
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-894-344C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쉼
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-621-976-15579/C
US-09-621-976-15579/C
Sequence 15579 Application US/09621976
Patent No. 663963
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Obbert, S.
TITLE OF INVENTION:
FILE REPERENCE: GENSET.054FR2
CURRENT APPLICANTION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 15579
LENGTH: 446
         TITLE OF INVENTION: ESTs and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SSOFWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                FEATURE:

NAME/KEY: CDS

LOCATION: 67..1390

LOCATION: 67..126

COTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 8.3999961853027

CUTER INFORMATION: seq AVVGCLLVPPAEA/NK

US-09-621-976-1416
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.2%; Score 16.6; D
Best Local Similarity 82.6%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.6; Di
Pred. No. 91;
0; Mismatches
                        FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1416
LENGTH: 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 GAAGGCCATGTAGAGCAACAGGG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389 GAAGGCCATGTAGAGCAACAGGG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAATCCATGTAAAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 181, Application US/09621976 Patent No. 6639063 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.61
Matches 19; Conservative
                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-621-976-181/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                        Length 9621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 292;
                                                                                 ; OTHER INFORMATION: Use of n signifies any of g, a, c or t US-09-125-028-1
                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: modified_base
LOCATION: (47)
OTHER INFORMATION: a, c, g, t, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: a, c, g, t, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (273)
J: OTHER INFORMATION: a, c, g, t, unknown or other US-09-720-655B-3
                                                                                                                                               Query Match
74.8%; Score 17.2; D
Best Local Similarity 86.4%; Pred. No. 94;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YAZAKI, MADOKA
APPLICANT: WATSUMOTO, KAYO
APPLICANT: TAKAYAMA, KIYOSHI
APPLICANT: TSURITANI, KATSUKI
TITLE OF INVENTION: SUGAR TRANSPORTER
FILE REFERENCE. ASA-C034
CURRENT APPLICATION NUMBER: US/09/720,655B
CURRENT FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: JP 10/187235
PRIOR APPLICATION NUMBER: JP 10/187235
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 72.2%; Score 16.6; D
Best Local Similarity 82.6%; Pred. No. 83;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                         7927 AAATTAATGTAAAGCACCAGGG 7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GAAGTGAATGCAAAGCAGCAGGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-621-976-1416/c
Sequence 1416, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: diordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                     2 AAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-09-720-655B-3/C
US-09-720-655B-3/C
Sequence 3, Application US/09720655B
Patent No. 6723521
GENERAL INFORMATION:
APPLICANT: YOSHIMOTO, MAKOTO
APPLICANT: YAZAKI, MAKOTA
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (36)
OTHER INFORMATION: a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: modified_base
                    FEATURE:
NAME/KEY: misc feature
LOCATION: (9318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ö

. 0

ö

Gaps

```
RESULT 15
US-09-673-395A-3/C
19-673-395A-3/C
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
72.2%; Score 16.6; DB 4; Length 1571;
Best Local Similarity 82.6%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0;
                                                                         Query Match 72.2%; Score 16.6; DB 4; Length 1416; Best Local Similarity 82.6%; Pred. No. 1.2e+02; Matches 19; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 5, 2004, 07:17:53
Job time : 4.864 secs
                                                                                                                                                                                                                                                                                                                                                                                     836 GAAATCCAGGAAAAGCAGAAGAG 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433 GAÁGGCCATGTAGAGCAACAGGG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                 1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
US-09-107-532A-2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-673-395A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2051, Application US/09107532A
Sequence 2051, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BNIEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESSES
GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USER
ZIE: 02354
COMPUTER READABLE FORM:
MEDIUM TYRE: CD/ROM ISO9660
COMPUTER: PC
COMPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.2%; Score 16.6; E
Best Local Similarity 82.6%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1416
SEQUENCE DESCRIPTION: SEQ ID NO: 2051:
                                                                                                                                                                                                        NAME/KEY: CDS
| NAME/KEY: CDS |
| LOCATION: 309..542 |
| NAME/KEY: sig_peptide |
| LOCATION: 309..455 |
| OTHER INFORMATION: Von Heijne matrix |
| OTHER INFORMATION: score 5.0999990463257 |
| OTHER INFORMATION: seq_LLYMAFLMLGGFS/DP |
| US-09-621-976-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 gaaggccargrangagcaacaggg 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-107-532A-2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                     LENGTH: 542
                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ö

Gaps

..

ö

Gaps

; 0

This Page Blank (uspto)

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

December 5, 2004, 06:58:29 ; Search time 330.898 Seconds (without alignments) 6907.991 Million cell updates/sec Run on:

US-09-698-903B-10 416 Title: Perfect score: Sequence:

1 ctacggcaatgtaccagctg..........catgaacacccaaactcgat 416

3694831 segs, 2747406616 residues Searched:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications NA:*

1. /cgn2_6/ptodata/2/pubpna/USO7_pUBCOMB.seq:*
2. /cgn2_6/ptodata/2/pubpna/DCT_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 5, Appli	Sequence 5, Appli	Sequence 4, Appli	Seguence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 24, Appl	Sequence 24, Appl	Sequence 13, Appl	Sequence 100, App
ID	US-10-027-880-5	US-09-509~945-5	US-09-509-945-4	US-09-733-151-2	US-10-375-332-2	US-09-733-151-1	US-10-375-332-1	US-09-970-921-7	US-09-733-151-24	US-10-375-332-24	US-10-047-542-13	US-10-047-542-100
DB	15	σ	σ	Q	15	σ	15	σ	σ	15	13	13
Query Match Length DB	7599	6233	6548	4832	4832	4946	4946	5349	1077	1077	4465	6602
Query Match	46.3	45.7	45.7	45.6	45.6	45.6	45.6	45.6	43.0	43.0	37.2	37.2
Score	192.6	190	190	189.6	189.6	189.6	189.6	189.6	179	179	154.6	154.6
Result No.	, 	8	m	Ω	Ω Ω	9	7	ω υ	σ υ	. c 10	11	12

equence equence quence 4 quence 4	equence 2 equence 2 equence 2	000	4 2	(4 (4 (4	(1 (1 (1	9 H G		Sequence 9, Appli Sequence 9, Appli Sequence 39, Appl Sequence 39, Appl Sequence 36, Appl Sequence 36, Appl Sequence 16, Appl
US-10-047-542-1 US-10-047-542-1 US-09-847-057-4 US-09-874-926-4	US-10-250-821-2 US-10-250-553-2 US-10-250-821-2	US-10-250-5 US-10-250-8 US-10-250-5	US-09-948-138-4 US-10-033-190-5 US-10-407-845A-	US-10 US-10 US-10	US-10-250 US-10-250 US-10-250	US-10-250-821-2 US-10-250-553-2 US-10-033-190-3	US-U9-794-384A- US-10-801-550- US-10-047-542- US-09-940-550A	
113	10 10 10	16 16	13	16 16	16 16	119	101	10 10 10 17
7129 8074 8340 8340	12079 12079 12085	12085 12093 12093	12241 12241 12241	13002	13905 15430 15430	17752 17752 10078	831 831 7129 9901	11978 12438 694 694 909 163382
4444	444	44.4	444	444	444	227	ი. 4. დ. ი. ი. თ. თ.	6. 24. 4. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6.
ต์ต์ ต์	ก์ก์ก	יי ייי ייי	mmm	in in in	. m m m	1 11 11 11 11 11	m m m 01	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
54.6 54.6 6.6 6.6 6.6		444					45.6 45.6 23.8	8.8 8.8 101 101 99 99 4.5
11 12 15 15 15 15 15 15 15 15 15 15 15 15 15	15 15	152	151	217	1446	2000	1 1 1 1 2 4 4 2	111
113 114 154	17 18	222	12 2 2 1 16 4 10	27.0	900	1266	34 34 38	6 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6
υυυυ	υυυ	טטט	,	υυι	000	0.0	Ü	000000

ALIGNMENTS

NS-10-027-880-5

| Sequence 5, Application US/10027880
| Sequence 5, Application No. US20030106105A1
| GENERAL INFORMATION:
| APPLICANT: HOFFMAN, BEATE
| TITLE OF INVENTION: PROMOTER EXPRESSED SPECIFICALLY IN PLANT ROOT CELLS,
| TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS CELLS CONTAINING SUCH A
| TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS CELLS CONTAINING SUCH A
| TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS CELLS CONTAINING SUCH A
| TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS CONTAINING SUCH A
| FILE REFERENCE: CHEP: 003US
| CURRENT APPLICATION NUMBER: US/10/027, 880
| PRIOR APPLICATION NUMBER: PCT/FR00/01768
| PRIOR APPLICATION UNMBER: PCT/FR00/01768
| PRIOR FILING DATE: 2000-06-23
| NUMBER OF SEQ ID NOS: 7
| SEQ ID NO 5
| LENGTH: 7599 TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: T-DNA of pGKBS
US-10-027-880-5

ö 6579 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 6638 9 1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 0; Gaps Query Match
Best Local Similarity 99.5%; Pred. No. 1.1e-29;
Matches 192; Conservative 1; Mismatches 0; Indels 0; <u>p</u> ò

g

N

```
Sequence 2, Application US/09733151
Patent No. USZO010029620A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10375332
Publication No. US20030188347A1
Publication No. US20030188347A1
APPLICANT: De Both, et al.
ITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
                                                                                                                                                                                                                                                                                        5471 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 6530
                                                ö
                                                                                                                                                                                                                     6411 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 6470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                         1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                              6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTTAAACTTGC
                                                                                                                                                                            61 ATCAATAAAWITAIGITITIGCITIGGACTATAATACCIGACTIGITATITIATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATCAATAAAWITATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                               TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4832;
45.7%; Score 190; DB 9; Length 6548; 99.0%; Pred. No. 3.6e-29; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
45.6%; Score 189.6; DB 9;
Best Local Similarity 99.5%; Pred. No. 3.9e-29;
Matches 189; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(4832)
CTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                               5531 GACCATGTACGT 6542
Query Match
Best Local Similarity 99.0
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                 181 GACCATGTACAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GACCATGIAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-733-151-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-10-375-332-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4832
                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEO ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                              d
                                                                                                                                                                                                              g
                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                 ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                     Sequence 5, Application US/09509945

Patent No. US20020166140A1

GENERAL INFORMATION:
TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
TITLE REPERENCE: 0230-0148P

CURRENT APPLICATION NUMBER: US/09/509,945

CURRENT PILING DATE: 2001-04-01

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 5

SEQ ID NO 5

SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09509945

Batent No. US20020166140A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
FILE REPERENCE: 0230-0148P

CURRENT FILING DATE: 2001-04-01

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 4

LENGTH: 6548
                                                           6699 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 6758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6342 CTACGCCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATCAATAAAWTTATGTTTTTGGACTATAATACCTGACTTGTTATTTTTATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATTTAAAACTATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTTCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 45.7%; Score 190; DB 9; Length 6539; Best Local Similarity 99.0%; Pred. No. 3.6e-29; Matches 190; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Escherichia coli LE392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
OTHER INFORMATION: Clone: pTS431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
CTHER INFORMATION: Clone: pTS172
US-09-509-945-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Escherichia coli LE392
                                                                                                                                     181 GACCATGTACATC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5522 GACCATGTACGT 6533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GACCATGTACAT 192
                                                                                                                                                                                                                 RESULT 2
US-09-509-945-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-509-945-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-509-945-4
                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                         g
                                                                                                       8 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
183 ATCAATAAATTTATGTTTTGCTTGGACTATAATACCTGACTTGTATTTTATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.5%; Pred. No. 4e-29;
Matches 189; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQUENCE TO APPLICATION US/09970921

PATCH NO. US2002013845A1

GENERAL INFORMATION:

TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2428-0108P

CURRENT APPLICATION NUMBER: US/09/970,921

CURRENT APPLICATION NUMBER: US/09/970,921

SOFTWARE: PATCHING DATE: 2001-10-05

SOFTWARE: PATCHING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LCCATION: (1)..(4946)
; OTHER INFORMATION: Plasmid pTHW107
US-10-375-332-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GACCATGTAC 190
                                                                                                                                                                                        181 GACCATGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GACCATGTAC 54
                                                                                                                                                                                                                                         63 GACCATGTAC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-970-921-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MS-09-733-151-1/C
Sequence 1. Application US/09733151
Sequence 1. Application US/09733151
Sequence 1. Application US/09733151
Sequence No. USZ0010029620A1
GENERAL INFORMATION:
TILLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
TILLE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT APPLICATION NUMBER: US/08/12-08
PRIOR PILING DATE: 1999-12-08
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TATITAAACTATATTICTITCAAGAAGGAATTAACAICTACAAATTGCCTITICTTAIC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTTTTATCAATAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.6%; Score 189.6; DB 9; Length 4946; Best Local Similarity 99.5%; Pred. No. 4e-29; Matches 189; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
45.6%; Score 189.6; DB 1:
Best Local Similarity 99.5%; Pred. No. 3.9e-29;
Matches 189; Conservative 1; Mismatches 0
        FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/10/375,332
CURRENT FILING DATE: 2003-02-27
FINCH APPLICATION NUMBER: US/09/733,151
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
LENGTH: 4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:

NAME/KEY: misc feature

LOCATION: (1). (4946)

OTHER INFORMATION: Plasmid pTHW107
US-09-733-151-1
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature; DCATION: (1)..(4832)
US-10-375-332-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GACCATGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACCATGTAC 54
```

q

ద

δ

ð

В ò g ò

ò

ö 120 121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTTCTTATC 180 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTTCGAATTTAAACTTGC 184 124 121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180 09 64 123 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTTCTTATC 64 183 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTTTTCAATAAA 61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 123 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC

us-09-698-903b-10.rnpb

```
q
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ор
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: De BOCh, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEG ID NO 24
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCAATAAAWTTATGTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 ATCAATAAATTTATGTTTTGCTTGGACTATAATACCTGGCTTGTTATTTTATCAATAAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAMEKRY: misc feature
LOCATION: Complement (1884)..(2258))
OTHER INFORMATION: Jabel = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus"
NAMEKRY: misc feature
LOCATION: (2281)..(3369)
OTHER INFORMATION: Jabel = PE1, "promoter of E1 gene of rice (WO
OTHER INFORMATION: 92/13956)"
                                                        OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "T-DNA of pTTS243"
                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((98)..(331))
OTHER INFORMATION: label = 3'97, "region containing 3' untranslated
OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: Complement((332)..(883))
OTHER INFORMATION: label = bar, "region coding for phosphinthricin
OTHER INFORMATION: acetyl transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 189.6; DB 9; Length
Pred. No. 4.1e-29;
1; Mismatches 0; Indels
                                                                                            NAME/KEY: misc_feature
LOCATION: CompTement((1)..(25))
OTHER INFORMATION: label = RB, "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 24, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACCATGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACCATGTAC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-733-151-24/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Бb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
GENERAL INVOCATION.

GENERAL INVOCATION.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REPERBREE: 514412-2019

CURRENT APPLICATION NUMBER: US/10/375,332

CURRENT FILING DATE: 2003-02-27

PRIOR APPLICATION NUMBER: 09/457,037

PRIOR FILING DATE: 1009-12-08

PRIOR FILING DATE: 09/457,037

PRIOR PLING DATE: 09/457,037

PRIOR PLING DATE: 1999-12-08

SOFTWARE: Patentin version 3.0

SEQ ID NO 24

LIENGTH: 1077
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                        1060 CTACGGCGATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                   941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 940 TATTTAAACTATATTTCTTTCAGAAGTGGGAATTAACATCTACAAATTGCCTTTTCTTATC 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      881
                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                    NAME/KEY: misc_feature

| LOCATION: (1)...(1077)

| OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1

US-09-733-151-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(1077)
; CTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
US-10-375-332-24
                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC
                                                                                                                                                                                                                                                                                          1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                        61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1060 CTACGGCGATGTACCAGCTGATATATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000 ATCAATAAATTTATGTTTTTGCTTGGACTATAATAACCTGACTTGTTATTTTATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAAACTTGC
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1077;
                                                                                                                                                                                         Score 179; DB 9; Length 1077; Pred. No. 3.7e-27; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 179; DB 15;
Pred. No. 3.7e-27;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 24, Application US/10375332; Publication No. US20030188347A1; GENERAL INFORMATION:
                                                                                                                                                                                         Query Match
Best Local Similarity 98.9%;
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.9%;
Matches 179; Conservative
TYPE: DNA
ORGANISM: Brassica napus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               880 G 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 G 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-10-375-332-24/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
```

```
SCHEMENT 121-100, Application US/10047542

| SEQUENCE 100, Application US/10047542
| Publication No. US2020168847A1
| GENERAL INFORMATION:
| APPLICANT: LARRICK, JAMES W. |
| APPLICANT: MYCOFF, KEITH L. |
| TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL |
| TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING OFFICE OFFIC
                                                                                                                                                                                     Sequence 13, Application US/10047542;
Publication No. US20020168367A1;
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL INMUNOADHESINS FOR TREATING AND PREVENTING VIRAL;
TITLE OF INVENTION: NOVEL INMUNOADHESINS FOR TREATING AND PREVENTING VIRAL;
TITLE OF INVENTION: NOVEL INMUNOADHESINS FOR TREATING AND PREVENTING VIRAL;
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFRENCE: 030905.0004.CIP1
CURRENT FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATCHILL OF THE SEQ ID NOS: 101
SEQ ID NOS: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3579 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATTTTTCTGAATTTAAACTTGC 3638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATCAATAAAWITATGITITIGCITGGACTATAATACCTGACTTGTTATTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTACGCCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.2%; Score 154.6; DB 13; Length 4465; 99.4%; Pred. No. 5.9e-22; tive 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Expression-type plasmid pBMSF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rarraaacrararrrrrrrraagargggarraa 3733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified base
LOCATION: (2214)...[2215)
CTHER INFORMATION: a, c, t or
US-10-047-542-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: a, c, t or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.4<sup>a</sup>
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: NAME/KEY: modified_base LOCATION: (2150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-10-047-542-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4465
                                                                                                                                RESULT 11
US-10-047-542-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
g
```

```
Sequence 101, Application US/10047542

| Sequence 101, Application NS. US2020168367A1
| Publication No. US2020168367A1
| GENERAL IRPORMATION:
| APPLICANT LARRICK, JAMES W. |
| APPLICANT: WYOOFF, KEITH L. |
| TILE OF INVENTION: NOVEL IMMUDADHESINS FOR TREATING AND PREVENTING VIRAL FILE OF INVENTION: AND BACTERIAL DISEASES |
| FILE REFERENCE: 03095.0004.CIP1 |
| CURRENT PELLOATION NUMBER: 2001-04-26 |
| PRIOR FILING DATE: 2001-04-28 |
| PRIOR PELLING DATE: 2000-04-28 |
| PRIOR FILING DATE: 2000-04-28 |
| NUMBER OF SEQ ID NOS: 101 |
| SEQ ID NO 101 |
| LENGTH 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                      5775
                                                                                                                                                                                                                                                                                                                                                                                           61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            887 CTACGGCANGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 827 Archarartrandritraccingacianaraccidacricianiriarcaaraa 768
                                                                                                                                                                                                                                                                                                                                                             61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
                                                                                                                                                                                                                                                                             1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTTAAACTTGC
                                                                                                                                                                                                                                                                                                                      5716 cracescraterecascreararararicastrarreaararricesarrraaacrree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; Length 7129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                             Length 6602;
                                                                                                                                                                                      Score 154.6; DB 13; Length
Pred. No. 6.7e-22;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Description of Unknown Organism:
) OTHER INFORMATION: pGPTV-hpt-ocs-35SJ/SC
US-10-047-542-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.2%; Score 154.6; DB 13; Best Local Similarity 99.4%; Pred. No. 6.9e-22; Matches 154; Conservative 1; Mismatches 0;
                                                                                  FEATURE:
OTHER INFORMATION: Description of Unknown Organism:
OTHER INFORMATION: pGPTV-kan-ocs-ATR-IgA2
US-10-047-542-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          767 TATTTAAACTATTTTCTTTCAAGATGGGAATTAA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAA 155
                                                                                                                                                                                         Query Match
Best Local Similarity 99.4%;
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
SEQ ID NO 100
LENGTH: 6602
TYPE: DNA
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-10-047-542-101/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

RESULT 14 US-10-047-542-14/c ; Sequence 14, Application US/10047542

```
6588 ATCAATAAATTTATGTTTTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 6529
                                                                                                                                                 6528 TATTTAAACTATATTTCTTTCAAGATGGGAATTAA 6494
                                                                                          121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAA 155
                                                                                                                                                                                                                                                                                           Search completed: December 5, 2004, 09:36:22 Job time : 331.898 secs
                                                                                                                                                      g
                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: AGRINOMICS, LLC.
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLAN
FILE REFERENCE: PAGODA
CURRENT APPLICATION NUMBER: US/09/847,057
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
                                                       JAPELICANT: LARRICK, JAMES W.
APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
JITLE OF INVENTION: NOTE. INVUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIPI
CURRENT APPLICATION NUMBER: US/10/047.542
CURRENT FILING DATE: 2000.04-28
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
SPRIOR PILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
PRIOR FILING DATE: 2000.04-28
SOFTWARE: Batentin Ver. 2.1
SEQ ID NO 14
CHARLES OF SEQ ID NO 14
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6648 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 6589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   887 CTACGCCARTGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTTTCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AICAATAAAWITAIGITITIGCIIGGACTAIAATACCIGACITGIIAITITIAICAAIAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTACGGCAATGTACCAGCTGATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 154.6; DB 13; Length 8074;
Pred. No. 7.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.2%; Score 154.6; DB 9; Length 8340; Best Local Similarity 99.4%; Pred. No. 7.2e-22; Matches 154; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Expression-type plasmid pBMSP-1spJSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        767 TATTTAAACTATATTTCTTTCAAGATGGGAATTAA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
37.2%; Score 154.6;
Best Local Similarity 99.4%; Pred. No. 7.2e
Matches 154; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09847057
Patent No. US20020004943A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
; ORGANISM: Binary vector pAGI4002
US-09-847-057-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: modified_base
COTHEN (2315)
USHORWATION: a, c, t or g
Publication No. US20020168367A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-847-057-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 05:20:20; search time 69.888 Seconds

(without alignments)

4230.886 Million cell updates/sec

Title: US-09-698-903B-10

Perfect score: 416
Sequence: 1 ctacggcaatgtaccagctg......catgaacacccaaactcgat 416
Scoring table: IDENTITY_NUC
Gapext 1.0
Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0 0 Maximum Match 00%
Post-processing: Minimum Match 100%
Listing first 45 summaries
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

lssued_Patents NA:*
1: \cgn2_6\ptodata1/\ina\5A\comB.seq:*
2: \cgn2_6\ptodata1/\ina\5B\comB.seq:*
3: \cgn2_6\ptodata1/\ina\6A\comB.seq:*
4: \cgn2_6\ptodata1/\ina\6B\comB.seq:*
5: \cgn2_6\ptodata1/\ina\PtoTUG\comB.seq:*
6: \cgn2_6\ptodata1/\ina\PtoTUG\comB.seq:*
6: \cgn2_6\ptodata1/\ina\PtoTUG\comB.seq:*

Database :

STIMMARTES

			* 6			SUMMARIES	
99.9 416 4 US-09-430-497A-10 Sequence 10, 46.3 5864 3 US-09-430-497A-8 Sequence 4, 46.3 5864 3 US-09-480-497A-8 Sequence 4, 46.3 5864 3 US-09-480-497A-1 Sequence 4, 46.3 5865 4 US-09-480-497A-1 Sequence 1, 45.7 5548 3 US-08-497A-1 Sequence 1, 45.7 7311 3 US-08-497A-1 Sequence 1, 45.7 7311 3 US-08-498-093-1 Sequence 2, 45.6 1303 3 US-08-498-093-2 Sequence 2, 45.6 1303 3 US-08-498-093-2 Sequence 2, 45.6 3200 1 US-08-498-093-2 Sequence 2, 45.6 432 4 US-09-737B-2 Sequence 2, 45.6 4946 3 US-08-497-037B-2 Sequence 1, 45.6 4946 4 US-09-737B-1 Sequence 1, 45.6 5349 3 US-08-497-037B-1 Sequence 1, 45.6 5349 3 US-08-497-037B-1 Sequence 1, 45.6 5349 3 US-09-733-151-1 Sequence 1, 45.6 5360 3 US-08-497-037B-1 Sequence 1, 45.6 5864 3 US-09-733-151-1 Sequence 1, 45.6 5864 3 US-09-430-497A-1 Sequence 1, 45.6 5864 3 US-08-312-016-23 Sequence 2, 45.6 5864 3 US-08-232-016-23 Sequence 2, 45.6 5864 3 US-08-532-016-23 Sequence 2, 45.6 5864 3 US-08-532-016-23 Sequence 2, 45.6 5864 3 US-08-532-016-23 Sequence 2, 45.7 5864 3 US-08-84-440-4 Sequence 2, 45.7 5864 3 US-08-84-440-4 Sequence 2, 45.7 5864 3 US-08-854-608-894-440-4 Sequence 2, 45.7 5864 3 US-08-854-440-4 Sequence 2, 45.7 5864 3 US-08-854-608-894-440-4 Sequence 2, 45.7 5864 3 US-08-854-864-8 Sequence 2, 45.7 5864 3 US-08-854-840-4 S	Score		Match	Length	DB.	ΩΙ	Description
91.5 415 4 US-09-430-497A-8 Sequence 8, 46.3 5864 3 US-09-430-497A-1 Sequence 4, 46.3 5864 3 US-09-430-497A-1 Sequence 4, 46.3 5865 4 US-09-430-497A-1 Sequence 1, 45.7 5548 3 US-08-894-440-1 Sequence 1, 45.7 5548 3 US-08-894-440-1 Sequence 1, 45.7 7 811 2 US-08-894-440-2 Sequence 1, 45.7 7 813 3 US-08-894-840-2 Sequence 2, 45.6 1303 3 US-08-894-840-2 Sequence 2, 45.6 1303 3 US-08-894-804-23 Sequence 2, 45.6 1303 0 US-08-894-804-23 Sequence 2, 45.6 4832 4 US-09-737B-2 Sequence 2, 45.6 4946 3 US-09-737B-1 Sequence 2, 45.6 4946 3 US-09-731-151-2 Sequence 1, 45.6 4946 4 US-09-731-151-1 Sequence 1, 45.6 5349 3 US-08-817-188-1 Sequence 1, 45.6 5360 3 US-08-817-188-1 Sequence 1, 45.6 5864 3 US-09-733-151-1 Sequence 1, 45.6 5864 3 US-09-733-151-1 Sequence 1, 45.6 5864 3 US-09-70-921-7 Sequence 1, 45.6 5864 3 US-09-817-188-5 Sequence 2, 45.6 5864 3 US-09-817-188-5 Sequence 2, 45.6 5864 3 US-09-817-188-5 Sequence 2, 45.6 5864 3 US-08-817-188-5 Sequence 2, 45.6 5	415.6	l lo	99.9	416	4	US-09-430-497A-10	10,
46.3 5864 3 US-08-894-440-4 46.3 5864 3 US-08-894-440-4 46.3 5864 4 US-09-458-093-4 45.7 6548 3 US-08-894-440-1 45.7 6548 3 US-08-894-440-1 45.7 6548 3 US-08-817-188-2 45.6 1303 3 US-08-849-680A-5 45.6 1303 3 US-08-894-440-2 45.6 1303 3 US-08-894-410-2 45.6 1303 3 US-08-894-410-2 45.6 1303 3 US-08-894-410-2 45.6 1303 3 US-08-894-410-2 45.6 4832 4 US-09-457-0378-1 45.6 4946 4 US-09-457-0378-1 45.6 5349 3 US-08-817-188-1 58quence 1, 58quence 1, 45.6 549 4 US-09-430-430-437-1 45.6 5864 3 US-08-431-1 45.6 5864 3 US-08-817-188-5 58quence 1, 45.6 5864 3 US-08-817-188-5 58quence 1, 58quence 1, 45.6 5864 3 US-08-817-188-5 58quence 2, 45.6 5864 3 US-08-823-016-23 58quence 2, 45.6 5864 3 US-08-824-40-4 58quence 2, 45.7 5864 3 US-08-824-40-4 58quence 2, 45.7 5864 3 US-08-824-40-4 58quence 2, 45.7 5864 3 US-08-824-40-4 58quence 2, 45.8 5864 3 US-08-824-40-4 58quence 2, 45.8 5864 3 US-08-824-40-4 58quence 2, 45.8 5864 3 US-08-824-40-4 58quence 2, 45.9 58	380.8	m	91.5	415	4	US-09-430-497A-8	8
46.3 5864 3 US-09-458-093-4 46.3 5865 4 US-09-458-093-4 45.7 6548 3 US-08-84-440-1 45.7 6548 3 US-08-81-440-1 45.7 6548 3 US-08-81-1-188-2 45.6 1303 3 US-08-81-1-1-1 45.6 1303 3 US-08-81-2-1 45.6 4832 4 US-08-81-1-1 45.6 4946 4 US-09-457-0378-1 45.6 4946 4 US-09-457-0378-1 45.6 5349 3 US-08-817-188-1 45.6 5349 3 US-08-817-188-1 45.6 5349 3 US-08-817-188-1 45.6 5349 3 US-08-817-188-1 45.6 5564 4 US-09-430-031-7 45.6 566 3 US-08-817-188-5 45.7 566 2 US-08-817-188-5 45.8 566 3 US-08-817-188-5 45.8 566 3 US-08-817-188-5 564 0 US-08-81	192.6	ø	46.3	5864	m	US-08-894-440-4	4
46.3 5865 4 US-09-430-497A-1 Sequence 1, 45.7 6548 3 US-09-430-440-1 Sequence 1, 45.7 6548 3 US-09-430-440-1 Sequence 1, 45.7 6548 3 US-09-458-093-1 Sequence 1, 45.7 7 8111 2 US-08-549-680A-5 Sequence 2, 45.6 1303 3 US-09-458-093-2 Sequence 2, 45.6 1303 3 US-09-458-093-2 Sequence 2, 45.6 3200 2 US-08-694-824-23 Sequence 2, 45.6 3200 2 US-08-694-824-23 Sequence 2, 45.6 4946 3 US-09-457-037R-2 Sequence 1, 45.6 4946 3 US-09-457-037R-1 Sequence 1, 45.6 4946 4 US-09-733-151-1 Sequence 1, 45.6 5349 3 US-09-068-101-7 Sequence 1, 45.6 5360 3 US-08-817-188-1 Sequence 1, 45.6 5865 4 US-09-733-151-1 Sequence 1, 45.6 5865 3 US-08-817-188-5 Sequence 2, 45.6 5864 3 US-08-817-188-5 Sequence 2, 45.7 5864 3 US-08-818-188-188-188-188-188-188-188-188-	192.6	9	46.3	5864	ო	US-09-458-093-4	4
0. 45.7 6548 3 US-08-894-440-1 Sequence 1, 10.0 45.7 6548 3 US-08-817-188-2 Sequence 1, 10.0 45.7 6548 3 US-08-817-188-2 Sequence 2, 10.0 45.7 7811 2 US-08-549-680A-5 Sequence 5, 13.0 3 US-08-944-40-2 Sequence 5, 13.0 3 US-08-945-400-2 Sequence 5, 13.0 3 US-08-453-104-23 Sequence 2, 10.0 08-453-104-23 Sequence 2, 10.0 08-457-0378-2 Sequence 2, 10.0 08-457-0378-1 Sequence 2, 10.0 08-457-0378-1 Sequence 2, 10.0 08-457-0378-1 Sequence 1, 10.0 08-457-0378-1 Sequence 2, 10.0 08-457-0378-1 Sequence 2, 10.0 08-457-0378-2 Sequence 2, 10.0 08-232-016-2 Sequence 2, 10.0 08-232-016-2 Sequence 2, 10.0 08-232-016-2 Sequence 2, 10.0 08-232-016-2 Sequence 2, 10.0 08-457-0378-2 Sequence 2,	192.6	ω.	46.3	5865	4	US-09-430-497A-1	H
0 45.7 6548 3 US-00-4817.188-2 Sequence 2, or 45.7 6548 3 US-09-458-093-1 Sequence 1, sequence 1, sequence 2, or 45.6 1303 3 US-09-458-093-2 Sequence 2, sequence 2, or 45.6 3200 10S-09-458-093-2 Sequence 2, sequence 2, or 45.6 3200 10S-09-458-093-2 Sequence 2, sequence 2, or 45.6 45.6 4832 4 US-08-453-104-23 Sequence 2, or 45.6 45.6 4832 4 US-09-453-104-23 Sequence 2, or 45.6 45.6 4832 4 US-09-457-037B-2 Sequence 2, or 45.6 45.6 4946 4 US-09-457-037B-1 Sequence 1, or 45.6 45.6 4946 4 US-09-457-037B-1 Sequence 1, or 45.6 45.6 5349 4 US-09-457-037B-1 Sequence 1, or 45.6 5549 4 US-09-450-031B-1 Sequence 1, or 45.6 5549 4 45.6 5569 4 45.6 5569 4 45.6 566 4 45.6 566 45.6 566 45.6 566 45.6 566 566 45.6 566 45.6 <td< td=""><td>H</td><td>190</td><td>45.7</td><td>6548</td><td>ო</td><td>US-08-894-440-1</td><td>4</td></td<>	H	190	45.7	6548	ო	US-08-894-440-1	4
0 45.7 6548 3 US-09-458 093-1 sequence 1 0 45.7 7811 2 US-08-549-680A-5 sequence 5, 6 45.6 1303 3 US-09-458-093-2 sequence 2, 6 45.6 3200 2 US-08-458-093-2 sequence 2, 6 45.6 4832 4 US-08-458-093-2 sequence 2, 6 45.6 4832 4 US-08-457-031-2 sequence 2, 6 48.6 480-6 3 US-08-817-188-1 sequence 2, 6 45.6 4946 4 US-09-781-151-1 sequence 1, 6 45.6 4946 4 US-09-768-101-7 sequence 1, 6 45.6 5349 3 US-09-068-101-7 sequence 1, 6 45.6 5360 3 US-09-08-101-7 sequence 1, 6 45.6 5560 3 US-09-08-11-7 sequence 2, 6 45.6 566 4 US-09-08-11-7 sequence 2, 6 45.6 566 4 US-09-08-11-7 sequence 2,	H	90	45.7	6548	٣	US-08-817-188-2	۲,
6 45.7 7811 2 US-0B-549-680A-5 Sequence 5, 645.6 1303 3 US-0B-844-40-2 Sequence 2, 645.6 1303 3 US-0B-458-093-2 Sequence 2, 645.6 3200 1 US-0B-453-104-23 Sequence 2, 645.6 4832 4 US-09-457-037B-2 Sequence 2, 645.6 4842 4 US-09-457-037B-1 Sequence 2, 645.6 4946 4 US-09-733-151-2 Sequence 1, 645.6 5349 3 US-0B-817-18B-1 Sequence 1, 645.6 5349 3 US-09-68-101-7 Sequence 1, 645.6 5560 3 US-0B-101-7 Sequence 1, 645.6 5560 3 US-0B-101-1 Sequence 2, 645.6 5863 4 US-0B-101-7 Sequence 2, 645.6 5863 3 US-0B-101-2 Sequence 2, 645.6 5864 3 US-0B-232-016-2 Sequence 2, 645.6 5864 3 US-0B-245-093-4 Sequence 2, 645.6 5864 3 US-0B-24	Ä	9	45.7	6548	ᠬ	US-09-458-093-1	-
6 45.6 1303 3 US-00-894-440-2 6 45.6 1303 3 US-09-458-093-2 6 45.6 3200 1 US-09-458-093-2 6 45.6 3200 2 US-08-453-104-23 6 45.6 4832 4 US-09-457-037B-2 6 45.6 4832 4 US-09-457-037B-2 6 45.6 4946 3 US-09-457-037B-1 6 45.6 4946 4 US-09-457-037B-1 6 45.6 5349 3 US-09-457-037B-1 6 45.6 5349 3 US-09-68B-101-7 6 45.6 5565 4 US-09-978-11-7 6 45.6 5565 4 US-09-978-11-7 6 45.6 5565 4 US-09-978-11-7 6 45.6 5565 4 US-09-970-921-7 6 45.6 5565 4 US-09-970-921-7 6 45.6 5565 4 US-09-970-921-7 6 45.6 5567 3 US-08-817-18B-5 6 45.6 5667 4 US-09-430-497-4 6 45.7 568 2 US-08-817-18B-5 6 45.6 5667 3 US-08-817-08-818-8 6 45.2 5864 3 US-08-818-440-4 7 5640-60-6 23, 7 7 4 US-09-457-037B-4 7 5640-60-6 24, 7 7 7 4 US-09-457-037B-4 7 5640-60-6 24,	ä	90	45.7	7811	7	US-08-549-680A-5	'n
6 45.6 1303 3 US-09-458-093-2 Sequence 2, 6 45.6 3200 1 US-08-694-824-23 Sequence 2, 6 45.6 3200 1 US-08-694-824-23 Sequence 2, 6 45.6 4832 4 US-09-457-037B-2 Sequence 2, 6 45.6 4832 4 US-09-457-037B-1 Sequence 2, 45.6 4946 4 US-09-457-037B-1 Sequence 1, 6 45.6 4946 4 US-09-457-037B-1 Sequence 1, 45.6 5349 3 US-09-068-101-7 Sequence 1, 45.6 5560 3 US-08-101-7 Sequence 5, 6 45.6 5560 3 US-08-101-7 Sequence 5, 6 45.6 5560 3 US-08-101-1 Sequence 2, 45.6 5560 3 US-08-101-1 Sequence 5, 6 45.6 5560 3 US-08-101-2 Sequence 2, 45.6 566 4 US-09-322-016-23 Sequence 2, 45.6 7566 2 US-08-232-016-23 Sequence 2, 45.6 7566 3 US-08-894-440-4 Sequence 2, 44.5 564 3 US-08-457-037B-24 Sequence 2, 44.5 564 3 US-09-457-037B-24 Sequence 2, 44.5 565 3 US-09-457-037B-24 Sequence 2, 44.5 56	189	٠	45.6	1303	m	US-08-894-440-2	۲,
6 45.6 3200 1 US-08-453.104-23 Sequence 23, 645.6 4832 4 US-09-457.037B-2 Sequence 23, 645.6 4832 4 US-09-457.037B-2 Sequence 2, 645.6 4946 3 US-09-857.037B-1 Sequence 2, 645.6 4946 4 US-09-733.151-2 Sequence 2, 645.6 4946 4 US-09-733.151-1 Sequence 1, 645.6 5349 3 US-09-68.101-7 Sequence 1, 645.6 5560 3 US-09-068.101-7 Sequence 1, 645.6 5560 3 US-09-17.18B-5 Sequence 7, 645.6 5560 3 US-09-17.18B-5 Sequence 2, 645.6 5865 4 US-09-31.01-7 Sequence 2, 645.6 5865 4 US-09-31.01-7 Sequence 2, 645.6 5865 4 US-09-440.4 Sequence 2, 645.6 5864 3 US-08-23.016-23 Sequence 2, 645.6 5864 3 US-08-23.016-23 Sequence 2, 645.6 5864 3 US-08-894.440-4 Sequence 2, 645.6 US-08-894.440-4	189	9	45.6	1303	m	US-09-458-093-2	ς.
6 45.6 3200 2 US-08.694-824-23 Sequence 23, 6 45.6 4832 4 US-09-457-037B-2 Sequence 23, 6 45.6 4832 4 US-09-457-037B-2 Sequence 23, 6 45.6 4946 3 US-09-817-188-1 Sequence 1, 6 45.6 4946 4 US-09-457-037B-1 Sequence 1, 6 45.6 5349 3 US-09-457-037B-1 Sequence 1, 6 45.6 5349 3 US-09-068-101-7 Sequence 7, 6 45.6 5560 3 US-08-071-7 Sequence 7, 6 45.6 5560 3 US-08-917-7 Sequence 7, 6 45.6 5560 3 US-08-917-7 Sequence 2, 6 45.6 5560 3 US-08-232-016-23 Sequence 2, 6 45.6 5560 3 US-08-232-016-23 Sequence 2, 6 45.6 5564 3 US-08-232-016-23 Sequence 2, 6 45.6 5564 3 US-08-894-440-4 Sequence 2, 6 45.6 5564 3 US-08-894-440-4 Sequence 2, 6 45.0 5662 4 US-09-457-037B-24 Sequence 2, 6 45.0 56	189.	9.	45.6	3200	Н	US-08-453-104-23	23.
6 45.6 4832 4 US-09-457-037B-2 Sequence 2, 6 45.6 4832 4 US-09-457-037B-2 Sequence 2, 6 45.6 4946 4 US-09-457-037B-1 Sequence 1, 6 45.6 4946 4 US-09-733-1151-1 Sequence 1, 6 45.6 5349 3 US-09-73-1151-1 Sequence 1, 6 45.6 5349 4 US-09-70-101-7 Sequence 1, 6 45.6 5349 4 US-09-70-91-7 Sequence 7, 6 45.6 5560 3 US-08-817-18B-5 Sequence 5, 6 45.6 5560 3 US-08-310-101-7 Sequence 2, 6 45.6 564 3 US-08-232-016-23 Sequence 2, 6 45.6 564 3 US-08-894-440-4 Sequence 2, 8 45.2 5864 3 US-08-894-440-4 Sequence 2, 8 45.2 5864 3 US-08-457-037B-24 Sequence 24, 8 45.2 5864 3 US-09-457-037B-24 Sequence 24, 8 45.2 5864	89.6	٩	45.6	3200	N	US-08-694-824-23	23,
6 45.6 4832 4 US-09-733-151-2 Sequence 2, 6 45.6 4946 3 US-09-733-151-1 Sequence 1, 6 45.6 4946 4 US-09-457-0378-1 Sequence 1, 6 45.6 4946 4 US-09-457-0378-1 Sequence 1, 6 45.6 5349 3 US-09-068-101-7 Sequence 1, 6 45.6 5349 4 US-09-970-931-7 Sequence 7, 6 45.6 5560 3 US-08-817-188-5 Sequence 5, 6 45.6 566 2 US-08-817-188-5 Sequence 5, 6 45.6 566 2 US-08-232-016-23 Sequence 2, 6 45.6 7566 2 US-08-232-016-23 Sequence 2, 6 45.6 7566 2 US-08-232-016-23 Sequence 2, 7838 45.2 5864 3 US-08-894-440-4 Sequence 2, 7845-2 5864 3 US-08-894-440-4 Sequence 2, 7856 2 US-08-53-03-24 Sequence 2	189	9.	45.6	4832	4	US-09-457-037B-2	~
6 45.6 4946 3 US-08-817-188-1 Sequence 1, 6 45.6 4946 4 US-09-457-037B-1 Sequence 1, 6 45.6 4946 4 US-09-457-037B-1 Sequence 1, 6 45.6 5349 3 US-09-068-101-7 Sequence 7, 6 45.6 5349 3 US-09-068-101-7 Sequence 7, 6 45.6 5560 3 US-09-970-921-7 Sequence 7, 6 45.6 5560 3 US-08-817-188-5 Sequence 1, 6 45.6 5562 4 US-09-430-437-1 Sequence 1, 6 45.6 7562 2 US-08-232-016-23 Sequence 2, 7564 3 US-08-232-016-23 Sequence 2, 7565 2 US-08-894-440-4 Sequence 2, 7565 2 US-08-894-440-4 Sequence 2, 7565 2 US-08-894-480-4 Sequence 2, 7565 2 US-08-894-480-4 Sequence 2, 7565 2 US-08-894-480-4 Sequence 2, 7565 2 US-08-894-880-780-780-780-780-780-780-780-780-780	83	9	45.6	4832	4	US-09-733-151-2	7
6 45.6 4946 4 US-09-457-037B-1 Sequence I. 6 45.6 4946 4 US-09-733-151-1 Sequence I. 6 45.6 5349 4 US-09-068-101-7 Sequence I. 6 45.6 5349 4 US-09-970-921-7 Sequence 7. 6 45.6 5560 3 US-08-817-188-5 Sequence 7. 6 45.6 5560 3 US-08-817-188-5 Sequence 2. 6 45.6 5560 3 US-08-232-016-23 Sequence 2. 6 45.6 7566 2 US-08-232-016-23 Sequence 2. 6 45.6 7566 2 US-08-232-016-23 Sequence 2. 7 8 45.2 5864 3 US-08-894-440-4 Sequence 2. 7 8 45.2 5864 3 US-08-945-093-4 Sequence 2. 7 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 45.2 5864 3 US-08-457-078-24 Sequence 2. 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8	9.	45.6	4946	m	US-08-817-188-1	H
6 45.6 4946 4 US-09-733-151-1 Sequence 1, 6 45.6 5349 3 US-09-068-101-7 Sequence 1, 6 45.6 5349 3 US-09-068-101-7 Sequence 7, 6 45.6 5560 3 US-08-817-188-5 Sequence 5, 6 45.6 5865 4 US-09-470-477A-1 Sequence 5, 6 45.6 5865 4 US-09-470-477A-1 Sequence 1, 6 45.6 7566 2 US-08-232-016-23 Sequence 22, 6 45.6 7566 2 US-08-232-016-23 Sequence 22, 8 45.2 5864 3 US-08-894-440-4 Sequence 4, 8 45.2 5864 3 US-08-894-440-4 Sequence 4, 8 45.2 5864 3 US-08-894-80-4 Sequence 24, 8 45.2 5864 3 US-08-457-078-24 Sequence 24, 8 45.2 5864 3 US-08-457-078-24 Sequence 24, 8 45.2 5864 3 US-09-457-078-24 Sequence 24, 8 45.2 5864 3 US-09-457-0778-24 Sequence 24, 8 45.2 5864 3 US-09-457-078-24 Sequen	189.6	9.	45.6	4946	4	US-09-457-037B-1	H
45.6 5349 3 US-09-068-101-7 Sequence 7, 45.6 5349 4 US-09-970-921-7 Sequence 7, 45.6 5360 3 US-08-817-188-5 Sequence 7, 45.6 5865 4 US-09-430-497A-1 Sequence 1, 45.6 5865 4 US-09-430-497A-1 Sequence 1, 45.7 566 2 US-08-232-016-23 Sequence 23, 45.6 759 2 US-08-232-016-24 Sequence 24, 45.2 5864 3 US-08-844-40-4 Sequence 24, 45.2 5864 3 US-08-844-60-4 Sequence 24, 43.0 1077 4 US-09-457-0378-24 Sequence 24,	189	ų,	45.6	4946	4	US-09-733-151-1	ij
6 45.6 5349 4 US-09-970-921-7 Sequence 7, 6 45.6 5560 3 US-08-817-188-5 Sequence 7, 6 45.6 5860 2 US-08-817-188-5 Sequence 1, 6 45.6 7566 2 US-08-232-016-23 Sequence 23, 6 45.6 7639 2 US-08-232-016-22 Sequence 22, 8 45.2 5864 3 US-08-894-440-4 Sequence 22, 8 45.2 5864 3 US-08-95-033-4 Sequence 24, 9 43.0 1077 4 US-09-457-0378-24 Sequence 24,	8	189,6	45.6	5349	m	US-09-068-101-7	7
6 45.6 5560 3 US-08-817-188-5 Sequence 5.6 45.6 5865 4 US-09-430-497A-1 Sequence 1, 6 45.6 7562 US-09-232-016-23 Sequence 22, 6 45.6 7639 2 US-08-232-016-22 Sequence 22, 8 45.2 5864 3 US-08-894-440-4 Sequence 24, 8 45.2 5864 3 US-09-458-093-4 Sequence 24, 9 43.0 10.77 4 US-09-457-0378-24 Sequence 24,	8	بو	45.6	5349	4	US-09-970-921-7	7
.6 45.6 5865 4 US-09-430-497A-1 Sequence 1, 6 45.6 7566 2 US-08-232-016-23 Sequence 23, 6 45.6 7568 2 US-08-232-016-23 Sequence 23, 8 45.2 5864 3 US-08-894-440-4 Sequence 4, 8 45.2 5864 3 US-08-894-440-4 Sequence 4, 8 45.2 5864 3 US-08-854-680-94, 8 45.2 5864 3 US-08-458-093-4 Sequence 4, 8 45.2 5864 3 US-08-457-0378-24 Sequence 24, 8 45.2 5864 3 US-08-457-0378-24 Sequence 24, 8 45.2 5864 3 US-08-457-0378-24	89	9.	45.6	5560	m	US-08-817-188-5	'n
.6 45.6 7566 2 US-08-232-016-23 Sequence 23, 6 45.6 7639 2 US-08-232-016-22 Sequence 22, 8 45.2 5864 3 US-08-894-440+ Sequence 4, 8 45.2 5864 3 US-09-458-093-4 Sequence 4, 9 43.0 1077 4 US-09-457-037B-24 Sequence 24,	89	9.	45.6	5865	4	US-09-430-497A-1	; ;
.6 45.6 7639 2 US-08-232-016-22 Sequence 22, 38 45.2 5864 3 US-08-894-440-4 Sequence 4, 45.2 5864 3 US-09-458-093-4 Sequence 24, 79 45.0 1077 4 US-09-457-0378-24 Sequence 24,	89	9.	45.6	7566	7	US-08-232-016-23	23
45.2 5864 3 US-08-894-440-4 Seguence 4, 45.2 5864 3 US-08-458-093-4 Seguence 24, 43 0 1077 4 US-09-457-037R-24 Seguence 24,	8	9.	45.6	7639	~	US-08-232-016-22	22
8 45.2 5864 3 US-09-458-093-4 Sequence 4, 2 9 43.0 1077 4 US-09-457-037B-24 Sequence 24,	H	88	45.2	5864	m	US-08-894-440-4	4
9 43.0 1077 4 US-09-457-037B-24 Seguence 24,	H	88	45.2	5864	m	US-09-458-093-4	
	13	6	43.0	1077	4	US-09-457-037B-24	24.

a

ò

6 B 6

Sequence 24, Appl Sequence 22, Appl Sequence 22, Appl Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli		AND METHOD FOR PRODUCING	nnce: 3' border MS-B2		16; 0; Gaps	TATTTCTGAATTTAAACTTGC 60 TATTTCTGAATTTAAACTTGC 60	actigitatitiatcaataa 120
4 US-09-733-151-24 1 US-08-453-104-22 2 US-08-654-824-22 4 US-09-874-055-4 4 US-09-874-926-4 4 US-09-874-926-4 1 US-08-674-138-4 1 US-08-674-138-4 1 US-08-476-015-2 3 US-09-044-189-2 4 US-09-080-625-3 4 US-09-080-625-3 4 US-09-685-782-2 4 US-09-685-782-2 4 US-09-685-782-2 4 US-09-685-782-2 4 US-09-685-782-2 4 US-09-685-782-2 4 US-09-685-782-2 4 US-09-685-782-2 4 US-09-685-782-2 5 US-09-685-782-2 6 US-09-685-782-2 7 US-09-685-782-2	ALIGNMENTS	ASSICA PLANTS	ence ption of Artificial Sequence ng region of elite event MS-1	DNA	%; Score 415.6; DB 4; 0%; Pred. No. 1.9e-93; 0; Mismatches 0;	ctacggcaatgtaccagctgatataatcagttattgaaatattctgaa 	atcaataaawitatgititigcitiggactataataccigactigitatititatcaataaa
42.5 3201 42.5 3201 42.5 3201 37.2 8340 36.7 11186 36.7 11186 36.7 11186 36.7 11186 35.0 3153 35.0 3153 35.0 3153 35.0 3336 35.0 3336 35.0 3336	-10 Application US/ S0951E	TOW, Brigit TOW, Brigit ION: MALE- ION: SAME 514412-20 TION WUMBER DATE: 1999 DATE: 1999	equeque	NA nt	99.9 Similarity 100. 6; Conservative	TACGGCAATGTACCA TACGGCAATGTACCA	atcaataaawttatgt atcaataaawttatgt
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-430-497A-: ; Sequence 10; ; Patent No. 65 ; CENNERAL INFOR	APPLICANT: WES APPLICANT: WES APPLICANT: DE TITLE OF INVENT TITLE OF INVENT TITLE REFERENCE: CURRENT FILING CURRENT FILING NUMBER: OF SEQ I SOFTWARE: PAFE	SEQ ID NO 10 LENGTH: 41 TYPE: DNA ORGANISM: FEATURE: OTHER INFO OTHER INFO	LOCATION: (1). OTHER INFORMAT NAME/KEY: misc. LOCATION: (194 OTHER INFORMAT IS-09-430-497A-10	Query Match Best Local S Matches 416	Oy 1 C	Oy 61 A: Db 61 A:
	#D 4 4		- 1- 1- 1- 1- 1- 1- 1- 1-			С Д	О Д

g ઠે

ઠે

```
NAME/KEY: misc feature
LOCATION: Complement((5840)..(5864))
                                                                                                                                                                                                                                                                         5864
                                             US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
360
                                                                                           301 AIGTACATATATTATATGAACATGATTAATGCTTGTGAGTTGTTCTCTTCGTAAGAGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                         TIGCTIGGACTATAATACCTGACTTGTTATTTTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 AICAAIAAATITIATGITITIGGITIGGACTATAATACCTGACTIGITATITIATCAATAAA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 cccriscrirracarssarricricscracrarricraticarararara-cerar 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 AATGTACATATATATATGAACATGATTAATGCTTGTGAGTTGTTCTCATCCGTAAGAG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                               361 TTCAATATGTAATGGTGAAGAGTCAAAACCCAAAATCATGAACACCCAAACTCGAT 416
                                                       301 ATGTACATATATTATATGAACATGATTAATGCTTGTGAGTTGTTCTCATCCGTAAGAGT
                                                                                                                                                       116 AATGTACATATATATTATATGAACATGATTAATGCTTGTGAGTTGTTCTCATCCGTAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GACCATGTACATCCTACCATAATTATAATTATAATTATAATAC-TGAAACCATGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: 5' border OTHER INFORMATION: flanking region of elite event MS-B2 NAMB/KEY: misc.feature
LOCATION: (1)...(234)
NAMB/KEY: misc.feature
LOCATION: (235)...(315)
NAMB/KEY: misc.feature
LOCATION: (235)...(415)
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 ITTCAATATGTAATGGTGAAGAGTCAAAAACCCAAAATCATGAACACCCAA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.5%; Score 380.8; DB 4; Length 415; 98.5%; Pred. No. 6.7e-85; rive 1; Mismatches 3; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/430,497A;
CURRENT APPLICATION NUMBER: US/09/430,497A;
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
TURNET 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCAATAAAWTTATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.5
Matches 404; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-430-497A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
```

ઠે g du

δ

q

à gg à g

셤 ઠે

ઠે

ò

```
FEATURE:
NAME/KRY: misc_feature
LCCATION: Complement((3168)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyademylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTCO113 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: promoter of small subunit gene of Rubisco of OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
Sequence 4, Application US/08894440
Batent No. 6025546
GABREAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NMSCOR
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SISPID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: Complement((883)..(2608))
                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
```

```
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                        5620 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAATATTTCTGAATTATTAAACTTGC 5679
                                                                                                                                                                                                                                                                                              61 ATCAATAAAWITATGTTTTTTTTGGACTATAATACCTGACTTGTTATTTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                          121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                       1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 60
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: CompLement((13868)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTCO113
NAME/KEY: misc feature
LOCATION: Complement(11).(25)
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
NAME/KEY: misc feature
LOCATION: Complement(98).(310)
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
NAME/KEY: misc feature
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
NAME/KEY: misc feature
LOCATION: Complement(33).(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: region coding for phosphinothricin acetyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3 nos)
NAME/KEY: misc feature
LOCATION: Complement((3032)..(3367))
                                                                                                                                   0
                                                                           Query Match 46.3%; Score 192.6; DB 3; Length 5864; Best Local Similarity 99.5%; Pred. No. 2.2e-38; Matches 192; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco of
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: region coding for barnase of Bacillus OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NASON:
CURRENT APPLICATION NUMBER: US/09/456,093
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 08/694,440
PRIOR PLILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET. 2.0
OTHER INFORMATION: left border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09458093
Patent No. 6344602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5800 GACCATGTACATC 5812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GACCATGIACAIC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 4
LENGTH: 5864
     US-09-458-093-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
```

```
Sequence 1, Application US/09430497A

Sequence 1, Application US/09430497A

Patent No. 6509516

GENERAL INFORMATION:
APPLICANT: WESTON, Brigitte

APPLICANT: WESTON, Brigitte

APPLICANT: WESTON, MALE-STERILE BRASSICA FLANTS AND METHOD FOR PRODUCING

TITLE OF INVENTION: AAME

TITLE OF INVENTION: AAME

TITLE OF INVENTION: 1999-10-29

CURRENT APPLICATION NUMBER: US/09/430,497A

COURENT FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

LENGTH: 5865

TYPE: DNA

CREATE SEGS

CREATE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5680 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 5739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5681 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 5740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5740 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 5799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5621 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 5680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ATCAATAAAWTTATGTTTTGCTTGGACTATAATACCTGACTTGTTATTTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TATTTAAACTATATTTCTTTCAAGATGGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTTATCAATAAA 120
CCATION: (4924)...(5216)
CTHER INFORMATION: promoter of nopaline synthase gene of
CTHER INFORMATION: promoter of nopaline synthase gene of
CTHER INFORMATION: Agrobacterium T-DNA (Pnos)
COTION: (5217)...(5489)
COTHER INFORMATION: region coding for barstar of Bacillus
COTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc_feature
COCATION: (5490)...(5765)
COTHER INFORMATION: region containing polyadenylation signal of gene 7
CTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
NAME/KEY: misc_feature
CTHER INFORMATION: (5840)...(5864))
COTHER INFORMATION: left border of Agrobacterium T-DNA
US-09-458-093-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5620 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.3%; Score 192.6; DB 3; Length 5864; Best Local Similarity 99.5%; Pred. No. 2.2e-38; Matches 192; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of ; OTHER INFORMATION: plasmid pCO113
US-09-430-497A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 5865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

46.3%; Score 192.6; DB 4; Length EBest Local Similarity 99.5%; Pred. No. 2.2e-38;
Matches 192; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seoo caccardracarc selz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GACCATGTACATC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-430-497A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
```

4

Mon Dec

g ઠે d

ઠે

```
6471 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 6530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 6410
121 TATITTAAACTATATITCTTTCAGAAGGGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATCAATAAAWITAIGITTTIGCITIGGACIAIAATACCIGACITGITATITITAICAATAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence: plasmid PTS172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; LOCATION: (6263)..(6496); OCHER INFORMATION: 3'97: 3' untranslated region containing the CTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium; OTHER INFORMATION: T-DNA US-08-817-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((2019)..(2288))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: 9olyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
MAME/KEY: misc_feature
LOCATION: (4336)..(5170)
OTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
OTHER INFORMATION: Virus
                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08817188
Patent No. 6074876
GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
FILE REFERENCE: 2121-0127P
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
FRALIER PILING DATE: 1996-07-31
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.7%; Score 190; DB 3; Length 6548; Best Local Similarity 99.0%; Pred. No. 9.9e-38; Matches 190; Conservative 1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           El gene of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: Complement((5711)...(6262))
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: Complement ((2289)..(2624))
OTHER INFORMATION: barnase: region coding for barnase
FEATURE:
NAMES/KEY: misc feature
LOCATION: Complement ((2625)..(4313))
OTHER INFORMATION: PEI: promoter region of EI gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                       181 GACCATGTACAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 6548
                                                                                                                                                                                                                                                                      US-08-817-188-2
                                  a
                                                                                                  à
                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
        5741 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6411 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 6470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
OCATION: Complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: (4336)..(5710)
OTHER_INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (6263)..(6496)
OTHER INFORMATION: region containing polyadenylation signal for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.7%; Score 190; DB 3; Length 6548; Best Local Similarity 99.0%; Pred. No. 9.9e-38; Matches 190; Conservative 1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAME/KEY: misc feature
LOCATION: (5711)...(6262)
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                            Sequence 1, Application US/08894440

Patent No. 6025546;

GENERAL INFORMATION:

APPLICANT: PLANT GENETIC SYSTEMS N.V.

TITLE OF INVENTION: Method to obtain male sterile plants;
FILE REPERENCE: NNSCOR

CURRENT APPLICATION NUMBER: US/08/894,440;

CURRENT FILING DATE: 1997-11-12

NOWHER OF SEQ ID NOS: 4

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (vector)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El
OTHER INFORMATION: (PE1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(2003)
OTHER INFORMATION: pUC19 derived vector sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                      5801 GACCATGTACATC 5813
                                                                     181 GACCATGTACATC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6548
                                                                                                                                                                                                    RESULT 6
US-08-894-440-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH:
```

g ò

ò

```
6471 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 6530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Verson #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,680A
FILING DATE: 16 JANUARY 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 20,330
REFERENCE/DOCKET NUMBER: 2121-0111P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CORNELISSEN, MARCUS
APPLICANT: CORNELISSEN, ARLETTE
APPLICANT: COSSELS, ARLETTE
APPLICANT: GOSSELS, PRENIGUE
APPLICANT: VAN ARRSEN, ROEL
TITLE OF INVENTION: MARKER GENE
NUMBER OF SEQUENCES:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
SITRET: P.O. Box 747
CITY: Falls Church
SITRET: VISA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER REAABALE FORM:
MEDIUM TYRE: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPANING SYSTEM: PC-DOS/MS-DOS
COPPRAING SYSTEM: PC-DOS/MS-DOS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 194..718
OTHER INFORMATION: /note= "T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: complement (729..1340)
LOCATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_recomb
LOCATION: 1..7811
OTHER INFORMATION: /label= vector pTRVA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: promoter
LOCATION: 1341..1756
OTHER INFORMATION: /label= 358 promoter
FBATURE:
                                                                                                                                                                                                                                                                                                       US-08-549-680A-5/c; Sequence 5, Application US/08549680A; Patent No. 5962768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 248345
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 7811 base pairs
TYBE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8050
                                                                                                                                                                          6531 GACCATGTACGT 6542
                                                                                                               181 GACCATGTACAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
TELEX: 2
                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                      셤
                                                    임
                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6411 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTTTTCAATAAA 6470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                      6471 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 6530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TATITAAACTATATTICITICAAGAIGGGAATTAACAICTACAAATIGCCTITICITAIC 180
                    61 ATCAATAAAWTTATGTTTTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 60
                                                                                                                      TATITIAAACTATATITICITICAAGATGGGAATTAACAICTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
NAME/KEY: misc_feature
LOCATION: (1). (2003)
OTHER INFORMATION: pUC19 derived vector sequences (vector)
NAME/KEY: misc_feature
LOCATION: Complement (2019)..(2283))
OTHER INFORMATION: 3, nos: region containing polyadenylation signal
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: COMplement((2284)...(2624))
COTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc_feature
LOCATION: COMPLEMENT((2625)...(4313))
OTHER INFORMATION: promoter of the stamen-specific El gene of rice
OTHER INFORMATION: (PE1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (4336)..(5710)
UNTER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
NAME/KEY: misc_feature
LOCATION: (571I)..(6262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/09458093; Patent No. 6344602; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: PLANT GENERIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants; FILE REPRENCE: NMSCOR.
; CURRENT APPLICATION UNMBER: US/09/458,093; CURRENT FILING DATE: 1999-12-10; PRIOR APPLICATION UNMBER: 08/894,440; PRIOR PLLICATION NUMBER: 08/894,440; NUMBER OF SEQ ID NOS: 4; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 1; LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.0%; Pred. No. 9.9e-38;
Matches 190; Conservative 1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                        6531 GACCATGTACGT 6542
                                                                                                                                                                                                                                                          181 GACCATGTACAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-458-093-1
                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                           쉱
                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                           g
                                                                                                                             ò
```

```
NAME/KEY: misc_feature
LOCATION: 484..684..684
OTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: polyadenylation region of I-DNA gene 7"
```

us-09-698-903b-10.rni

```
1158 ATCAATAAATITTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 1217
            ô
                                                                                                  1098 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 1157
                                                                                                                                                                                                                                                                                1218 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1098 CTÁCGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1158 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTTTTATAAA 1217
                                                                                                                                                     120
                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI
OTHER INFORMATION: Eragment of pT988
OTHER INFORMATION: Geature
IOCATION: (1)._(35)
OTHER INFORMATION: Dolylinker of pGEM2 (pGEM2)
NAME/KEY: misc_feature
IOCATION: (36)._(694)
OTHER INFORMATION: 355 promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: M1841 (P355)
NAME/KEY: misc_feature
IOCATION: (655)..(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                  61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA
                                                                                                                                                                                                                                             TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (968)...(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Facebace 2, Application US/09458093
; Patent No. 6344602
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REPERENCE: NMSCOR
; CURRENT PELING DATE: 1999-12-10
; CURRENT FILING DATE: 1999-12-10
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIN Ver. 2.0
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.6%; Score 189.6; DB 3; Best Local Similarity 99.5%; Pred. No. 8.7e-38; Matches 189; Conservative 1; Mismatches 0;
       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1288)..(1303)
; OTHER INFORMATION: polylinker of pGEM2 US-09-458-093-2
            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
       189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        1278 GACCATGTAC 1287
                                                                                                                                                                                                                                                                                                                                          181 GACCATGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-458-093-2
                                                                                                                                                                                                                                             121
       Matches
                                                                                             g
                                                                                                                                             à
                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                        570
                                                                                                                                                                                                                                                                                                                                        FGCTTGGACTATAATACCTGACTTGTTATTTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                   121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                               509 TATTTAAACTATATTTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 450
                                                                                                                                                                                                                                             09
                                                                                                                                                                                                                                                                         1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HindIII-EcoRI
OTHER INFORMATION: fragment of pTS88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (36)-(694)
OTHER INFORMATION: 355 promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.6%; Score 189.6; DB 3; Length 1303; 99.5%; Pred. No. 8.7e-38;
                                                                                                                                     Query Match 45.7%; Score 190; DB 2; Length 7811; Best Local Similarity 99.0%; Pred. No. 1e-37; Matches 190; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08894440;
Patent No. 6025546;
GENERAL INPRRAITION:
TITLE OF INVENTION: Method to obtain male sterile plants;
FILE REFERENCE: NMSCOR;
CURRENT APPLICATION NUMBER: US/08/694,440;
CURRENT APPLICATION NUMBER: US/08/694,440;
NUMBER OF SEQ ID NOS: 497-11-12;
NUMBER OF SEQ ID NOS: 420-11-12;
SEQ ID NO 2;
SEQ ID NO 2;
LENGTH: 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: (695)...(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
; NAME/KEY: misc_feature
; LOCATION: 3001..3023
OTHER INFORMATION: /note= "T-DNA left border
; OTHER INFORMATION: sequences"
US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (1). (35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

LOCATION: (1288)..(1303)

CTHER INFORMATION: polylinker of pGEM2

US-08-894-440-2
                                                                                                                                                                                                                                                                                                                                     61 ATCAATAAAWTTATGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GACCATGTACAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         449 GACCATGTACGT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (968). (1287)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-894-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180

```
Sequence 23, Application US/08694824

Sequence 23, Application US/08694824

Patent No. 5897306

GENERAL INFORMATION:

APPLICANT: CONTRELISSEN, Marc

APPLICANT: STAM, Maike

A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2952 CTACGGCALGTACCAGCTGALALAALCAGTLATTGAATATTTCTGAATTTAAACTTGC 3011
                                                                                                                                                                       3012 ATCAATAAATTTATGTTTTGGTTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 3071
                                                                                                            121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria STATE: Virginia COUNTR: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 2078-12082
OTHER INFORMATION: \(\note=\) \(\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.5%; Pred. No. 1.1e-37;
Matches 189; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09-AUG-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: GB 90401055.0
FILING DATE: 18-APR-1990
ATTORNEY, AGENT INFORMATION:
NAME: Rea, Teresa S
REGISTRATION NUMBER: 30,427
REPERRENCE/DOCKET NUMBER: 30,427
REPERRENCE/DOCKET NUMBER: 1010830-032
FILEPHONE: (703) 836-6220
TELEPHONE: (703) 836-6221
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                           3132 GACCATGTAC 3141
                                                                                                                                                                                                                                                                                                                          181 GACCATGIAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-08-694-824-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                               8
                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: CORRELISESNY, MATC
APPLICANT: SCEPARETY Piet
APPLICANT: SCEPARETY STAM, Waise
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
ITTLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
INTERED CONDENCES: 23
CORRESSONDENCES: 23
CONDETES READABLE FORM:
ADDITOR TYPE: Ploppy disk
COMPUTER READABLE FORM:
ADDITOR TYPE: Ploppy disk
COMPUTER: ISP PIC-OS/MS-DOS
COMPUTER: ISP PIC-OS/MS-DOS
COMPUTER: ISP PIC-OS/MS-DOS
COMPUTER: TEMPC-COMPATION BRIAS: US /09/453,104
FILING DATE: GB 90401055.0
ATDIANTON NUMBER: US /09/453,104
ATDIANTON NUMBER: 108 90401055.0
ATDIANTON NUMBER: 108 90401055.0
ATDIANTON NUMBER: 30,427
APPLICATION NUMBER: 30,427
RETERBANCE/DOCKET NUMBER: 30,42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2952 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 3011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AICAATAAAWITAIGITITIGCIIGGACTATAATACCIGACTIGITATITATCAATAAA 120
                     1218 TATITAAACTATATTTCTTTCAAGAATTAACATCTACAAATTGCCTTTTCTTATG 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
45.6%; Score 189.6; DB 1; Length 3200;
Best Local Similarity 99.5%; Pred. No. 1.1e-37;
Matches 189; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: /note= "Nucleotides 2078-2082; OTHER INFORMATION: wherein N is not known."
US-08-453-104-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/08453104
Patent No. 5633446
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature LOCATION: 2078..2082
                                                                                                                                                                                                                                                                                                    1278 GACCATGTAC 1287
                                                                                                                                                                                                  181 GACCATGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-08-453-104-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                 엄
                                                                                                                                                                                                        ò
```

ω

```
Search completed: December 5, 2004, 07:17:52 Job time : 69.888 secs
     1999-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GACCATGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACCATGTAC 54
PRIOR FILING DATE: 19:
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin vei;
SEQ ID NO 2
LENGTH: 4832
                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: De Both, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
                                                                                                                                                                                                                                                                                                                         APPLICANT: De BOCH, et al.
TITLE CO INVENTION: HTBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/457,037B
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 099/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 4832
                                    3012 AICAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCATAAA 3071
                                                                                                         GTTATTTATCAATAAA 120
                                                                                  121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATCAATAAAWITATGTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 189.6; DB 4; Length 4832;
Pred. No. 1.2e-37;
1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)...(4832)
CTHER INFORMATION: T-DNA of Plasmid pTHW118
NAME/KRY: misc feature
LOCATION: (1883)..(4065)
COTHER INFORMATION: Hpa I restriction fragment
US-09-457-037B-2
                                                                                                                                                                                                                                        RESULT 14
US-09-457-037B-2/c
; Sequence 2, Application US/09457037B
; Betten No. 6506963
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09733151
Patent No. 6563026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                61 ATCAATAAAWTTATGTI
                                                                                                                                                                                      3132 GACCATGTAC 3141
                                                                                                                                                     181 GACCATGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACCATGTAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-733-151-2/c
                                                                                                                     3072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                            qq
                à
                                               임
                                                                               ò
                                                                                                                                                     ઠે
                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
61 AICAATAAAWITAIGITITIGGITIGGACTATAATACCIGACTIGITAITTAICAATAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                           Length 4832;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                     Query Match 45.6%; Score 189.6; DB 4; Best Local Similarity 99.5%; Pred. No. 1.2e-37; Matches 189; Conservative 1; Mismatches 0;
                                                                                                                                                                         NAME/KEY: misc feature
; LOCATION: (1)...(4832)
; OTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2
PatentIn version 3.0
                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
```

ö

184

ĕ

```
TYPE: DNA ORGANISM: Artificial Sequence
10077
3201
3201
3340
8340
1186
1186
1186
1186
3153
3353
3353
3336
3336
3434
3440
 JS-09-430-497A-8
                                                                                                                                                                                                                                                                                                                                   US-09-430-497A-8
                                                                                                                                                                                                                                              SEQ ID NO 8
LENGTH: 415
61
                                                                                                                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                         FEATURE:
  0 0 0 0 0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                      Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                             Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                             ; Search time 69.72 Seconds (without alignments) 4230.886 Million cell updates/sec
                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    gtcgagtttggtgttcatga......cagctggtacattgccgtag 415
                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                /cgn2_6/ptodata/1/ina/5A_COMB.seg:*
/cgn2_6/ptodata/1/ina/5B_COMB.seg:*
/cgn2_6/ptodata/1/ina/6A_COMB.seg:*
/cgn2_6/ptodata/1/ina/6A_COMB.seg:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seg:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seg:*
        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                        US-09-430-497A-8

US-09-430-497A-10

US-08-894-404-4

US-08-891-440-1

US-08-817-440-1

US-08-817-440-2

US-08-458-093-1

US-08-458-093-1

US-08-458-093-1

US-08-458-093-2

US-08-458-093-2

US-08-458-093-2

US-08-457-0378-1

US-08-457-0378-1

US-09-733-151-1

US-09-733-151-1
                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                    824507 seqs, 355394441 residues
                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              2004, 05:20:20
                                 model
                                                                                                        Gapop 10.0 , Gapext 1.0
                                  3
                                                                                                                                                                                            Issued Patents NA:*
                                 using
                                                                                                                                              seq length: 0
seq length: 200000000
                                                                       US-09-698-903B-8
415
                                                                                                                                                                                                                                                                                                                 Length
                                               'n
                                                                                                  IDENTITY NUC
                                 nucleic search,
                                               December
                                                                                                                                                                                                                                                                                      Query
Match
                                                                                                                                                                                                                                                                                                         100.0
91.8
                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                 Scoring table:
                                                                                                                                              Minimum DB
Maximum DB
                                 nucleic
                                                                                      Sequence:
                                                                                                                     Searched:
                                                                                                                                                                                            Database
                                               Run on:
```

```
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGGATGAGAACAACTCACAAGCATTAATCATGTTCATATAAATATATGTACATTATAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09430497A

Patent NO. 6509516
GENERAL INFORMATION

APPLICANT: WESTON, Brigitte

APPLICANT: DE BEUCKELEER, Marc

TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING

TITLE OF INVENTION: SAME

FILE REPERRNCE: 514412-2020
CURRENT PAPLICATION NUMBER: US/09/430,497A

CURRENT FILING DARE: 1999-10-29

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                            Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GTATATATACACGTATACAAATAGTAGGGAAGAAATCCATGTAAAGCAGCAGGGGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ATGGTTTCAAGTATTATATAATTATAATTATAATTATGGTAGGATGTACATGGCCGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGTTTCAAGTATTATAATTATAATTATAATTATGGTAGGATGTACATGGCCGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCGAGITIGGIGITCAIGAITITGGGITTIGACICTICACCAITACAIAITGAAACICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATATATACACGTATACAAATAGTAGCGAAGAAATCCATGTAAAGCAGCAGGGGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTCGAGTTTGGTGTTTTTGGGTTTTGACTCTTCACCATTACATTGAAACTCT
                                                                                                            ecunance
sedimence
sedimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHER INFORMATION: Description of Artificial Sequence: 5' border OTHER INFORMATION: flanking region of elite event MS-B2 OTHER INFORMATION: flanking region of elite event MS-B2 LOCATION: (1)..(234) OTHER INFORMATION: plant DNA OTHER INFORMATION: plant DNA DIOCATION: (235)..(415) (415) OTHER INFORMATION: T-DNA
                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 4.2e-92;
Matches 415; Conservative 0; Mismatches 0;
US-09-733-151-24
US-08-453-104-22
US-09-847-057-4
US-09-948-128-4
US-09-948-118-4
US-09-948-118-2
US-09-948-118-2
US-09-948-121-2
US-09-044-121-2
US-09-08-2
US-09-69-782-3
US-09-69-782-3
US-09-69-782-3
US-09-69-782-3
US-09-69-782-3
US-09-69-782-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
```

241

4, 1 24, 1

Sequence

.09-458-093-4 .09-457-037B-24

Sequence

Sequence

Sequence

US-09-430-497A-1 US-08-232-016-23

υυ

0000000

```
NAME/KEY: misc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                         360
                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245
                     GAAAAGGCAATTTGTAGATGTTAATTCCCATCTTGAAAGAATATATAGTTTAAATATTTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 TATACACGTATACAAATAGTAGCGGAGAAAATCCATGTAAAGCAGCAGGGGGCACCATGGT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 TGAGAACAACTCACAAGCATTAATCATGTTCATATAAATATATGTACATTATAC-GTATA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-09-430-497A-10/C
US-09-430-497A-10/C
Sequence 10, Application US/09430497A
Factor No. 650516
GENERAL INFORMATION:
APPLICANT: WESTON Brigitte
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
FILE REPRENCE: 514412-2020
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT PILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAATAACAAGTCAGGTATTATAGTCCAAGCAAAACATAAATTTATTGATGCAAGTTTAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 AAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAAWTTTATTGATGCAAGTTTAA 51
                                                                                        TGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAAATTTATTGATGCAAG
                                                       TGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAAAATTTGATGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATACACGTATACAAATAGTAGCGAAGAAATCCATGTAAAGCAGCAGGGGGCACCATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAAGTATTATAATTATAATTATAATTATGGTAGGATGTACATGGCCGATAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 TITGGTGTTCATGATTTTGGGTTTTGACTCTTCACCATTACATATTGAAACTCTTACGGA
Gaps
                                                                                                                              361 ITTAAATICAGAAATAITICAAATAACIGATTAITATCAGCTGGTACATTGCCGTAG 415
                                                                                                                                                           361 TTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCAGABATATTTCABTABACTGATTATATACAGCTGGTACATTGCCGTAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 380.8; DB 4; Length 416;
Pred. No. 8.4e-84;
1; Mismatches 3; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: 3' OTHER INFORMATION: flanking region of elite event MS-B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.5%;
Matches 404; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

: LOCATION: (194).. (416)

: OTHER INFORMATION: plant DNA

US-09-430-497A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (1)..(193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 10
                                                                                          301
                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                      g
                                                                                                                              ઠે
                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
FEATURE:
NAME/KEY: misc feature
LOCATION COMPLEMENT((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (5490). (5765)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: T-DNA OTHER INFORMATION: plasmid pTCO113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: Complement((331),..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
US-08-894-440-4/c
; Sequence 4, Application US/08894440
; Sequence 4, Application US/08894440
; Patent No. 602546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants;
; TILE REFERENCE: NMSCAN.
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: region coding for barnase of Bacillus OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCA/KEY: misc_feature
LOCA/TGY: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: Complement((3032)..(3367))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
Complement((5840)..(5864))
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: 1
LOCATION: 0
```

```
SEQ ID NO 1
LENGTH: 5865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                            5692 TADATITIATIGAIGCAAGITIADATITCAGAAATATITICAATAACIGATIATATCAGCIGG 5633
                                                                                                                                                                                                                                                                                                               5752 TATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAACA 5693
                                                                                                                                                                                                                                                                   TATAGITIAAATATITIATIGATAAAATAACAAGICAGGIATIATAGICCAAGCAAAAACA 342
                                                                                                                                                                                                                                                                                                                                                                  TAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco of
OTHER INFORMATION: promoter of small subunit gene of Rubisco of
OTHER INFORMATION: Arabidopsis (Pseu)
NAME/KEY: misc feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: 13-nos)
OTHER INFORMATION: (3-nos)
NAME/KEY: misc feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc feature
LOCATION: complement((3032)..(3467))
OTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc feature
LOCATION: complement((3038)..(4877))
OTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc feature
COTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc feature
COTHER INFORMATION: amyloliquefaciens
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                  Score 191.4; DB 3; Length 5864; Pred. No. 1.4e-37; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: T-DNA (OTHER INFORMATION: plasmid pTCO113
NAME/KEY: misc feature
LOCATION: Complement(1)..(25)
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
NAME/KEY: misc feature
LOCATION: Complement(98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature_
LOCATION: Complement ((331)..(882))
OCHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants;
FILE REFERENCE: NASCOR
CURRENT APPLICATION NUMBER: US/09/458,093
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 08/894,440
PRIOR FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SEQ ID NOS: 4
LENGTH: 5864
, OTHER INFORMATION: left border of Agrobacterium T-DNA US-08-894-440-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09458093
Patent No. 6344602
                                                                     46.18;
99.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACATTGCCGTAG 415
                                                                     Query Match
Best Local Similarity 99.5
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-458-093-4/C
                                                                                                                                                                                                                                                                     283
                                                                                                                                                                                                                                                                                                                                                                    343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403
                                                                                                                                                                                                                                                                                                                                                                                                              업
                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
5693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATAGTITAAATAITITATIGATAAATAACAAGTCAGGTAITATATAGTCCAAGCAAAAACA 5694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5692 haarittatigargcaagrittaaritcagaaratitcaaraacigartarahcagcigg 5633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATAGITITAAATATTITATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 TATAGITITAAAITATTIGAIAAAATAACAAGICAGGIAITATAGICCAAGCAAAAACA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WESTON, Brigitte
APPLICANT: WESTON, Brigitte
APPLICANT: DE BEUCKELEER, Marc
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: ASMS
FILE REPERBORS: 514412-2020
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT FILIS DATE: 1999-10-29
SUPPRENT FILIS DATE: 1999-10-29
SUPPRENT FILIS DATE: 1999-10-29
SOFTWARE: PATENTIN US: 14
        COTHER INFORMATION: (4924)...(5116)
COTHER INFORMATION: promoter of nopaline synthase gene of
COTHER INFORMATION: Agrobacterium T-DNA (Pnos)
NAME/KEY: misc_feature
LOCATION: (5217)...(5489)
COTHER INFORMATION: region coding for barstar of Bacillus
COTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc_feature
LOCATION: (5490)...(5765)
COTHER INFORMATION: region containing polyadenylation signal of gene 7
COTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
NAME/KEY: misc_feature
LOCATION: Complement((5840)..(5864))
COTHER INFORMATION: left border of Agrobacterium T-DNA
US-09-458-093-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5752 TATAGITITAAATATTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 TAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAAATAACTGATTATATCAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence: T-DNA; OTHER INFORMATION: plasmid pC0113
US-09-430-497A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
46.1%; Score 191.4; DB 4;
Best Local Similarity 99.5%; Pred. No. 1.4e-37;
Matches 192; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
46.1%; Score 191.4; DB 3
Best Local Similarity 99.5%; Pred. No. 1.4e-37;
Matches 192; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-430-497A-1/c;
Sequence 1, Application US/09430497A;
Patent No. 6509516;
Patent No. 978MAIION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5632 TACATTGCCGTAG 5620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 TACATTGCCGTAG
feature
```

g ଚ

8

```
6422 AAAITTATIGATGCAAGITTAAATITCAGAAATATITCAATAACIGAITATATGAGCTGGT 6363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 ATAGTTTAAATATTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAACAT 343
                                 344 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 AIGTACAIGGCCGAIAAGAAAAGGCAAITIGIAGAIGIIAAITICCCAICIIGAAAGAAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Description of Artificial Sequence: plasmid PTS172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature;
COCATION: (6263)..(6496)
COTHER INFORMATION: 3'g7: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium;
COTHER INFORMATION: T-DNA
US-08-817-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRATURE.
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: Complement ((2019)..(2288))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (4336)..(5170)
CTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
OTHER INFORMATION: Virus)
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
TITLE OF INVENTION: QENETIC TRANSFORMATION USING A PARP INHIBITOR
CURRENT APPLICATION NUMBER: US/08/817,188
CURRENT PILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PT/FP96/03366
EARLIER PILING DATE: 1996-07-31
EARLIER PILING DATE: 1995-08-04
NUMBER: PATENTING DATE: 1995-08-04
SOFTWARE: PATENTING DATE: 1995-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%; Score 188.8; DB 3; Length 6548; 99.0%; Pred. No. 6.3e-37; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: Complement((5711)..(6262))
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: PEl: promoter region of El gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAMEN/KEX: misc_feature
NAMEN/KEX: misc_feature
LCCATION: Complement((2289)..(2624))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08817188; Patent No. 6074876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                        6362 ACATTGCCGTAG 6351
                                                                                                                                             404 ACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                   US-08-817-188-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Sim:
Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEO ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                      셤
                                                                                                                                                                                     셤
                              ઠ
                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                 5693 TABATTTATIGATGCAAGTTTABATTCAGAAATATTTCAATAACTGATTATATCAGCTGG 5634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6482 ATAGITIAAATATITIAITGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACAT 6423
343 TAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATATGAGCTGG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 ATAGITIAAATAITTAITGATAAAATAACAAGICAGGIAITATAGICCAAGCAAAAACAI 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: Description of Artificial Sequence: plasmid pTS174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fo gene 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOGATION: Complement((12625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El gene of rice
OTHER INFORMATION: (PEI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (4336)..(5710)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
FBATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 188.8; DB 3; Length 6548; Pred. No. 6.3e-37; 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: Complement(C1019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation s
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (5711)..(6262)
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: (6263)..(6496)
OTHER INFORMATION: region containing polyadenylation signal
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (vector)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc feature
LOCATION: Complement((2284)). (2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                     RESULT 6
US-08-894-440-1/c
US-08-894-440-1/c
; Sequence 1, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1). (2003)
OTHER INFORMATION: pUC19 derived vector sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative (
                                                                                                                                                                     sess racarrecerrae sesi
                                                                                                                 403 TACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORU
US-08-894-440-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
```

ð d ò

```
6422 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT 6363
                                                                                                                                                                                                                                                          US-08-549-680A-5; Sequence 5, Application US/08549680A
Sequence 5, Application US/08549680A
Setent No. 5962768; GENERAL INFORMATION;
                                                                                                                                                  sa62 ACATTGCCGTAG 6351
                                                                                            404 ACATTGCCGTAG 415
                                                                                                                                                                                                                                     RESULT 9
                                      음
                                                                                         δ
                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6482 ATAGTITAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACAT 6423
     6482 ATAGITIABARITITAITGARAAAAAAAAAGGAGGATAITATAGTCCAAGGAAAAAA 6423
                                                                                                                                6422 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATATCAGCTGGT 6363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 AIGTACATGGCCGATAAGAAAAGCAATITGTAGATGTTAATTCCCATCTTGAAAAAAT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 ATAGTTTAAATTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACAT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT 403
                                                                                               344 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTTCAATAACTGATTATATCAGCTGGT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (6263)...(6496)
COTHER INFORMATION: region containing polyadenylation signal fo gene 7
COTHER INFORMATION: of Agrobacterium T-DNA (3'97)
US-09-458-093-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)..(2003)
OTHER INFORMATION: pUC19 derived vector sequences (vector)
NAME/KEY: misc_feature
LOCATION: Complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: of nopaline synthase gene of Agrobacterium MAME/KEY: misc feature
LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
OTHER INFORMATION: deployed factors
LOCATION: Complement((2255)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El gene of rice OTHER INFORMATION: (PE1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature.

NAME/KEY: misc feature.

LOCATION: (4336)..(5710)

OTHER INFORMATION: 15S promoter of Cauliflower Mosaic Virus (P35S)

NAME/KEY: misc feature.

OTHER INFORMATION: region coding for phosphinothricin acetyl

OTHER INFORMATION: transferase (bar)

NAME/KEY: misc feature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5%; Score 188.8; DB 3; Length 6548; 99.0%; Pred. No. 6.3e-37; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                      US-09-458-093-1/c
; Sequence 1, Application US/09458093
; Sequence 1, Application US/09458093
; GENERAL INFORMATION:
    APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants;
    TITLE OF INVENTION: MASCOR
; CURRENT PILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 08/694,440
; PRIOR PILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTMARE: Patentin Ver. 2.0
; SEQ ID NO :
    LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                6362 ACATTGCCGTAG 6351
                                                                                                                                                                                                             404 ACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 190; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                  a
                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                  ò
```

```
NAME/KEY: misc_feature
LOCATION: 484..684
OTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: polyadenylation region of T-DNA gene 7"
FRATURE:
NAME/KEY: CDS
LOCATION: complement (729..1340)
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTMARE: Patentin Release #1.0, Verson #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,680A
FILLING DATE: 16 JANUARY 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REGISTRATION NUMBER: 2121-0111P
TELECHMONE: (703) 205-8000
APPLICANT: CORNELISSEN, MARCUS
APPLICANT: CORNELISSEN, MARCUS
APPLICANT: GOSSELE, VERONIQUE
APPLICANT: GOSSELE, VERONIQUE
APPLICANT: VAN ARRSEN, ROEL
TITLE OF INVENTION: MARKER GENE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bich, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Palls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: 194.718
OTHER INFORMATION: /note= "T-DNA right border"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: complement (729..1340)
OTHER INFORMATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_recomb
LOCATION: 1..7811
OTHER INFORMATION: /label= vector pTRVA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: promoter
LOCATION: 1341..1756
OTHER INFORMATION: /label= 35S promoter
FEATURE:
                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAX: (703) 205-8000
TELEN: (703) 205-8000
TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7811 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: circular
MOLECULE TYPE: DNA (synthetic)
FEATURE:
```

```
406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-458-093-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                           셤
                                                                                                                     ò
                                                                                                                                                           셤
                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                               403
                                                                                                                                                                                                                                                                                                                                                                                       558 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT 617
                                                                                                                                                                                                   284 ATAGITITAAATATITATIGATAAAATAACAAGICAGGIAITATAGICCAAGCAAAAACAT 343
                                                                                                                                                                                                                                     498 ATAGTTTAAATATTTATTGATAAATTAACAAGTCAGGTATTATAGTCCAAGGAAAAACAT 557
                                                                                                                                                                                                                                                                                                                                                             AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEATURE:
NAME/KEX: misc_feature
LOCATKEX: (1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI OTHER INFORMATION: fragment of pTS88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
NAME/KEY: (36)...(694)
OCATION: (36)...(694)
OTHER INFORMATION: 358 promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 188.4; DB 3; Length 1303; Pred. No. 5.6e-37;
                                                                                                                        Length 7811;
                                                                                                                   Score 188.8; DB 2; Length
Pred. No. 6.6e-37;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc feature
LOCATION: (955). (967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-894-440-2/c
US-08-894-440-2/c
; Sequence 2, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REPERENCE: NMSCOR
NAME/KEY: misc_feature
LOCATION: 3001..3023
LOCATION: 3001..3023
OTHER INFORMATION: \(\text{Ance} = \text{"T-DNA left border}\)
OTHER INFORMATION: \(\text{sequences}\)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/FEX: misc_feature
NAME/FEX: misc_feature
OCCATION: (1)._(35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature;

LOCATION: (1288)..(1303)

CHER INFORMATION: polylinker of pGEM2

US-08-894-440-2
                                                                                                                 45.5%;
Best Local Similarity 99.0%;
Matches 190; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acatricciciae 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                               ;
US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                               344
                                                                                                                                                                                                                                                                                                                                                                                                                                           404
                                                                                                                                                                                                                                   日
                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
ö
                                                                                                       1227 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAACATAA 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1227 AGTTTAAATATTTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 1168
                                                                                                                                                           345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 ATTIATIGATGCAAGTITAAATTCAGAATATTTCAATAACTGATTATATCAGCTGGTAC 405
                                                                                                                                                           286 AGTTTAAATTTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA
                                                                                                                                                                                                                                                                     346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATCAGCTGGTAC
                                                      Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI OTHER INFORMATION: fragment of pTS88
NAME/KEY: misc_feature
LOCATION: (1)...(35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (968)...(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
NAME/KEY: misc feature
LOCATION: (1288)...(1303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEX: misc feature
LOCATION: (36). (694)
OTHER INFORMATION: 24 promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: 24 promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: (957)
OTHER INFORMATION: (957). (967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.4%; Score 188.4; DB 3; Length 1303; Best Local Similarity 99.5%; Pred. No. 5.6e-37; Matches 189; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09458093

Fatent No. 6344602

GENERAL INFORMATION:
FILE OF INVENTION: Method to obtain male sterile plants

TITLE OF INVENTION: Method to obtain male sterile plants

TITLE OF INVENTION: MASCOR

CURRENT EMPERENCE: NMSCOR

CURRENT FAPPLICATION NUMBER: US/09/458,093

CURRENT FILING DATE: 1999-12-10

PRIOR FILING DATE: 1997-11-12

NUMBER OF SEQ ID NOS: 4

SEQ ID NOS: 4

SEQ ID NOS: 4

SEQ ID NOS: 4

SEQ ID NOS: 4
1; Indels
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INPORMATION: polylinker of pGEM2
US-09-458-093-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   1107 Arricceras 1098
```

유 à 셤

```
Sequence 23, Application US/08694824
Patent No. 5877306
GENERAL INFORMATION:
APPLICANT: SCEPARET, Piet
APPLICANT: SCEPARET, Piet
APPLICANT: SCEPARET, Piet
APPLICANT: STAM Marke
APPLICANT: STAM Marke
APPLICANT: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
NUMBER OF SEQUENCE: 23
CORRESPONDENCE ADDRESS:
                                                                                                                 3021 AITTATTGATGCAAGTITAAATTCAGAAAATTTTCAATAACTGATTATATATCAGCTGGTAC 2962
          3081 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAA 3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3141 GTÄCATGGTCGATÄAGÄÄÄÄAGGCÄÄTTTGTÄGATGTTÄÄTTTCCCATCTTGAÄGÄÄÄTÄT 3082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSEE: ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
45.4%; Score 188.4; DB 2; Length:
Best Local Similarity 99.5%; Pred. No. 6.8e-37;
Matches 189; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 2078...2082
OTHER INFORMATION: /note= "Nucleotides 2078-2082
OTHER INFORMATION: wherein N is not known."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 2078..2082
                                                                                                                                                                                                                                                               2961 ATTGCCGTAG 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                             406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                         US-08-694-824-23/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-694-824-23
                                                                      ò
                                                                                                                                          음
                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/08453104

APPLICANT: SORTARRT, Fiet

APPLICANT: STAM, Maik

APPLICANT: DOCK Jan

TITLE OF INVENTION: INDECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

TITLE OF INVENTION: INDECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

TITLE OF INVENTION: INDECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION

TITLE OF INVENTION: INDECTICIDAL - CRYSTAL PROTEIN GENES

ADPRESSED: BUTTS, Doane, Swecker & Mathis

STATE: J2313-1404

COMPRESSED BUTTS, Doane, Swecker & Mathis

STATE: J2313-1404

COMPUTER: IMP COMPATA: APPLICATION DATA: APPLICATION NUMBER: US/08/453,104

TLING DATE: APPLICATION DATA: APPLICATION NUMBER: US/08/453,104

TLING DATE: APPLICATION NUMBER: US/08/453,104

APPLICATION NUMBER: US/08/453,104

TELEBRANCH/GRANT INFORMATION:

TELEBRANCH/GRANT INFORMATION:

TELEBRANCH (703) 836-6620

TELEBRANCH (703) 836-6201

INFORMATION FOR ED. 1D NO: 23: SEQUENCE CLOSE SECONDATION: PRACE DESCTORMATION: POR ED. 201

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
286 AGTTTAAATTTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 3200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature;
| IOCATION: 2078..2082
| OTHER INFORMATION: /note= "Nucleotides 2078-2082;
| OTHER INFORMATION: wherein N is not known."
| US-08-453-104-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.4%; Score 188.4; DB 1; 99.5%; Pred. No. 6.8e-37; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.5
Matches 189; Conservative
                                                                                                                                                                          1107 ATTĠĊĊĠTAĠ 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                      406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                         RESULT 12
US-08-453-104-23/c
                                          1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

a 8

ð

```
completed: December 5, 2004, 07:17:52 ne : 70.72 secs
                                                 4832
                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search comp
Job time :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                            日
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
                                                                                                                                                                                                                                                                                                                       APPLICANT: De Both, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REPERENCE: 5.14412-2019
FILE REPERENCE: 5.14412-2019
CURRENT APPLICATION NUMBER: US/09/457,037B
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
                                                                                           3081 AGTTTAAATATTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTTTAAATATTTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 345
                                                                      346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTITAAATATITATIGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 ATTIATIGATGCAAGTITAAATTCAGAAATATTTCAATAACTGATTATATATCAGCTGGTAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTIATTGATGCAAGTITAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 AGITITAATITITITITITAAATAACAAGICAGGIAITATAGICCAAGCAAAAACATAA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.4%; Score 188.4; DB 4; Length 4832; Best Local Similarity 99.5%; Pred. No. 7.4e-37; Matches 189; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT DE BCCH, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEI
FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
                                                                                                                                                                                                                                                                     Sequence 2, Application US/09457037B; Patent No. 6506963; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-733-151-2
; Sequence 2, Application US/09733151
; Patent No. 6563026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                               2961 ATTGCCGTAG 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGCCGTAG 243
                                                                                                                                             406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4832
                                                                                                                                                                                                                                                        US-09-457-037B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                d
                                                                        ò
                                                                                                       d
                                                                                                                                           ઠે
                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
114 AGTTTAAATATTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 AGTTTAAATTTTTTTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA
                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                              45.4%; Score 188.4; DB 4; Length 4832; 99.5%; Pred. No. 7.4e-37; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                      FEATURE:

NAME/KEY: misc feature
LOCATION: (1). (4832)

OTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.5
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 ATTGCCGTAG 243
```

us-09-698-903b-8.rnpb

Run on:

```
December 5, 2004, 06:58:29; Search time 330.103 Seconds (without alignments) 6907.991 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-698-903B-8
415
1 gtcgagtttggtgttcatga......cagctggtacattgccgtag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7389662
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3694831 segs, 2747406616 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY NUC Gapoxt 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 5, Appli	Sequence 5, Appli	Seguence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Seguence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 24, Appl	Sequence 24, Appl	Sequence 13, Appl	Sequence 100, App
	σI	15 US-10-027-880-5	US-09-509-945-5	US-09-509-945-4	US-09-733-151-2	US-10-375-332-2	US-09-733-151-1	US-10-375-332-1	US-09-970-921-7	US-09-733-151-24	US-10-375-332-24	US-10-047-542-13	US-10-047-542-100
	0.0	15	σ	σ	σ	15	σ	15	σ	σ	15	13	13
	Query Match Length DB ID	7599	6239	6548	4832	4832	4946	4946	5349	1077	1077	4465	6602
₩	Query Match	46.1	45.5	45.5	45.4	45.4	45.4	45.4	45.4	43.2	43.2	37.3	37.3
	Score	191.4	188.8	188.8	188.4	188.4	188.4	188.4	188.4	179.4	179.4	155	155
	ult No.	н	7	m	4	Ŋ	9	7	œ	σ	10	11	12
	Result No.	ט	υ	υ								υ	υ

В

à g

44 4 H	4 153 35.9 10078 13 05-10-33-19-3 Sequence 7. 2 146 35.2 831 17 05-10-801-550-7 Sequence 7. 2 146 35.2 831 17 05-10-801-550-7 Sequence 7. 2 145 34.9 7129 13 US-10-047-542-101 Sequence 7. 2 12.6 29.5 9901 10 US-09-940-550A-11 Sequence 1. 2 117.6 28.3 11978 10 US-09-940-550A-11 Sequence 8. 17.6 28.3 11978 10 US-09-792-568-9 Sequence 9. 17.6 28.3 12438 10 US-09-792-568-9 Sequence 9. 2 101 24.3 694 91 US-09-733-131-39 Sequence 3. 3 97.4 23.5 909 15 US-10-375-332-36 Sequence 3. 3 97.4 23.5 909 15 US-10-375-332-36 Sequence 3. 5 13.7 69081 13 US-10-875-332-36 Sequence 3. 5 13.7 69081 13 US-10-875-332-36 Sequence 3. 5 13.7 69081 13 US-10-871-192.	RESULT 1 US-10-027-880-5/C US-20-027-880-5/C Sequence 5, Application US/10027880 Publication No. US20030106105A1 GENERAL INFORMATION: APPLICANT: HOFFRAN, BEATE TITLE OF INVENTION: PROMOTER EXPRESSED SPECIFICALLY IN PLANT ROOT CELLS, TITLE OF INVENTION: PROMOTER AND RECOMBINANT HOST CELLS CONTAINING SUCH A TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS OBTAINED TITLE OF INVENTION: US/10/027,880 CURRENT APPLICATION NUMBER: US/10/027,880 CURRENT APPLICATION NUMBER: E2001-12-21 PRIOR FILING DATE: 2000-06-23 PRIOR FILING DATE: 2000-06-23 NUMBER OF SEQ ID NOS: 7 SEQ ID NO 5 TYPE: DNA CRGANISM: Artificial Sequence FEATURE: DNA ORGANISM: Artificial Sequence CHER INFORMATION: Description of Artificial Sequence: T-DNA of pGXB5	Query Match 46.1%; Score 191.4; DB 15; Length 7599; Best Local Similarity 99.5%; Pred. No. 6.6e-30; Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
	2 M M M M M 4 4 4 4 4 4	RESULT OS-10-0 Sequence GENERAL APPL TITL TITL FILE CURR CURR PRIO PRIO SEQ I SEQ I TEN COGG COGG COGG COGG COGG COGG COGG COG	Query Best Match

```
Sequence 2, Application US/09733151
Sequence 2, Application US/09733151
Patent No. US20010029620A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DE BOCH, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR RILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: De Both, et al. IIILE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
                                                                                                                                                                                                    6423
                                        ô
                                                                                                                     6483
                                                                                                                                                                                                                                                                                 6422 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT 6363
                                                                                                                                                              343
                                                                                                                                                                                                                                             403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 AGTITAAATATITATIGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 173
                                                                                                             6482 ATAGTTTAAATATTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 ATAGTTTAAATTTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT
                                          Gaps
                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
Length 6548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.4%; Score 188.4; DB 9; Length 4832; 99.5%; Pred. No. 2.4e-29; tive 0; Mismatches 1; Indels 0;
                                        Indels
  Score 188.8; DB 9;
Pred. No. 2.2e-29;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1). (4832)
CTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10375332 Publication No. US20030188347A1 GENERAL INFORMATION:
Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                      404 ACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.5
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTGCCGTAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4832
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-733-151-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-10-375-332-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                    q
                                                                                                                     g
                                                                                                                                                              ò
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                   APPLICANT: HAMADA, Kazuyuki et al.
TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
FILE REPERENCE: 023-0148P
CURRENT APPLICATION NUMBER: US/09/509,945
CURRENT FILING DATE: 2001-04-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO S
LENGTH: 6539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09509945

Patent No. US20020166140A1

Patent No. US20020166140A1

APPLICANT: HAMADA, Kazuyuki et al.

TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
FILE REFERENCE: 0230-0148P

CURRENT APPLICATION NUMBER: US/09/509,945

CURRENT FILEM DATE: 2001-04-01

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1
                                                     6651 TAPATITTATIGATGCAAGTITAAATICAGAAATATITTACAATAACTGATTATATCAGCTGG 6592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6473 ATAGTITTAAATATTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACAT 6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6413 AAATITATIGAIGCAAGITIAAATICAGAAATATITCAATAACIGAITATATCAGCIGGI 6354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 ATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAAAAT 343
                       TAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATATCAGCTGG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 188.8; DB 9; Length 6539;
Pred. No. 2.2e-29;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                             ; Sequence 5, Application US/09509945; Patent No. US20020166140A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc feature
; OTHER INFORMATION: Clone: pTS431
US-09-509-945-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone: pTS172
US-09-509-945-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Escherichia coli LE392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Escherichia coli LE392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative (
                                                                                                                                           5591 TACATIGCCGTAG 6579
                                                                                                      TACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATTGCCGTAG 6342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATTGCCGTAG 415
                                                                                                                                                                                                       RESULT 2
US-09-509-945-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-509-945-4/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6353
                       343
                                                                                                      403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 4
                       ઠે
                                                         임
                                                                                                    \dot{\delta}
                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
```

```
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345
114 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 ATTIATIGAIGCAAGITIAAATICAGAAATATTICAATAACIGAITATATCAGCIGGIAC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 GTACATGGTCGATAAGAAAGGCAATTTGTAGAGTGTTAATTCCCATCTTGAAGAAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 AGTITAAATATITATIGATAAAATAACAAGICAGGTATIATAGICCAAGCAAAAACATAA
                                                       346 ALTIATIGATGCAAGTITAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAAATAACTGATTATATCAGCTGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.5%; Pred. No. 2.4e-29;
Matches 189; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09970921
; Sequence 7, Application US/09970921
; Parent No. US2002013845A1
; GENERAL INFORMATION:
APPLICANT: Frank Michiels et al.
; TILE OF INVENTION: Improved Barstar Gene; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION UNMEER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
; LENGTH: 5349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature; LOCATION: (1)..(4946); OTHER INFORMATION: Plasmid pTHW107US-10-375-332-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 ATTGCCGTAG 243
                                                                                                                                406 ATTGCCGTAG 415
                                                                                                                                                                234 Arreceras 243
                                                                                                                                                                                                                       RESULT 7
US-10-375-332-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-09-970-921-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       රි
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                           ò
                                                                                       g
                                                                                                                              ò
                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09733151
Patent No. US20010029620A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
KLOR APPLICATION NUMBER: 09/457,037
FRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATATGGGTAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 233
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                    Length 4832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.4%; Score 188.4; DB 9; Length 4946; Best Local Similarity 99.5%; Pred. No. 2.4e-29; Matches 189; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                Score 188.4; DB 15; Length
Pred. No. 2.4e-29;
0; Mismatches 1; Indels
   PILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/10/375,332
CURRENT FILING DATE: 2003-02-7
PRIOR APPLICATION NUMBER: US/09/733,151
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER: OF SEQ ID NOS: 43
SEQ ID NO 2
                                                                                                                                                                                                                                                                               , LOCATION: (1). T(4832)
, OTHER INFORMATION: Plasmid pTHW118
US-10-375-332-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LOCATION: (1). (4946)
, OTHER INFORMATION: Plasmid pTHW107
US-09-733-151-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.5%;
Matches 189; Conservative
                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 ATTGCCGTAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (1)..(4946)
                                                                                                                                                                                                                                                            NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-733-151-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286
                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

·.

us-09-698-903b-8.rnpb

```
1060 Ġ 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 G 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09733151

Sequence 24, Application US/09733151

GENERAL INFORMATION:

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME TITLE OF INVENTION: MAPRICA 12-2019

FILE REPERENCE: 514412-2019

CURRENT APPLICATION NUMBER: US/09/733,151

CURRENT FILING DATE: 2000-12-08

PRICR APPLICATION NUMBER: 09/457,037

PRICR PILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 AGTITAAATATITATIGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature: actu, "T-DNA tight border"

LOCATION: Complement((1)..(25))

GTHER INFORMATION: label = RB, "T-DNA right border"

NAME/KEY: misc feature

LOCATION: Complement((98)..(331))

GOTHER INFORMATION: label = 3'g7, "region containing 3' untranslated

COCATION: Complement((382)..(883))

GOTHER INFORMATION: acetyl transferase"

LOCATION: Complement((382)..(883))

GOTHER INFORMATION: acetyl transferase"

LOCATION: Complement((884)..(2258))

GOTHER INFORMATION: Virus"

NAME/KEY: misc feature

LOCATION: Complement((884)..(2258))

GOTHER INFORMATION: Virus"

NAME/KEY: misc feature

LOCATION: (2281)..(3959)

GOTHER INFORMATION: label = PEI, "promoter of El gene of rice (WO

COTHER INFORMATION: 1abel = PEI, "promoter of El gene of rice (WO

COTHER INFORMATION: 1abel = PEI, "promoter of El gene of rice (WO

COTHER INFORMATION: 1abel = PEI, "promoter of El gene of rice (WO

COTHER INFORMATION: 20113956)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAAACATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (4546). (4577)
OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
OTHER INFORMATION: end of chalcone synthase gene"
OTHER INFORMATION: Description of Artificial Sequence: other nucleic
OTHER INFORMATION: acid, "T-DNA of pTTS243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (3970)..(4245)
OTHER INFORMATION: label = synb*; "improved barstar DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 45.4%; Score 188.4; DB 9;
Best Local Similarity 99.5%; Pred. No. 2.5e-29;
Matches 189; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: Complement((5325)..(5349))
OTHER INFORMATION: label = LB, "T-DNA left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 ATTGCCGTAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Pa
SEQ ID NO 24
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-09-733-151-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

```
RESULT 10
US-10-375-332-24

i Sequence 24, Application US/10375332

publication No. UG20030188347A1

GENERAL INFORMATION:

APPLICANT DE BOACH, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME

TITLE OF INVENTY PAPLICATION NUMBER: US/09/733,151

PRIOR FILING DATE: 2000-12-08

PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 24

LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000 IGCAAGITIAAATICAGAAATAITITCAATAACIGATTATATCAGCIGGTACAICGCGTA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1000 TGCAAGTTTAAATTTCAGAAATATTTCAATAACTGATTATATCAGCTGGTACATCGCCGTA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294
                                                                                                                                                                                                                                                                                                                                                                      354
                                                                                                                                                                                                                                                                                                                                                                                                                  999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 TGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTACATTGCCGTA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAAATTTATTGA 354
                                                                 NAME/KEY: misc_feature; LOCATION: (1)..(1077)
COTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 US-09-733-151-24
                                                                                                                                                                                                                                                                                                              940 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAAATTTATTGA
                                                                                                                                                                                                                                                                              295 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAAATTTATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 TGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTACATTGCCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940 AITTATIGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAACATAAATTATTGA
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature

// Inccarion: (1)...(1077)

// OTHER INFORMATION: sequence comprising the 5' flanking region of

US-10-375-332-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,
                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 179.4; DB 15; Length 1077; Pred. No. 1.1e-27; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                  Length 1077;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                  Score 179.4; DB 9;
Pred. No. 1.1e-27;
                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                  Query Match
Best Local Similarity 99.4%;
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.4%;
Matches 180; Conservative
TYPE: DNA
ORGANISM: Brassica napus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Brassica napus
```

1060 G 1060

g

```
GENERAL INFORMATION:

Sequence 100, Application US/10047542

Publication No. US20020168367A1

GENERAL INFORMATION:

APPLICANT: LARRICK, JAMES W.

APPLICANT: WCOPF, KEITH L.

ITILE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

TITLE OF INVENTION: AND BACTERIAL DISEASES

FILE REFERENCE: 030905.0004.CIP1

CURRENT APPLICATION NUMBER: US/10/047,542

PRIOR PILING DATE: 2001-10-26

PRIOR PILING DATE: 2001-04-28

PRIOR PILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SOFTWARE: PATCHIN VOY: 2.1
US-10-047-542-13/C

is Sequence 13, Application US/10047542

publication No. US20020168367A1

igeneral INFORMATION: US20020168367A1

igeneral INFORMATION: Ames W.

igeneral INFORMATION: AMES W.

APPLICANT: LARRICK, TEITH W.

ITILE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

ITILE OF INVENTION: AND BACTERAL DISEASES

FILE REFERENCE: 030905.0004.CIPI

CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-026

PRIOR FILING DATE: 2001-04-28

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SEQ ID NO 13

LENGTH: 4465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 TATTATAGTCCAAGCAAAAAATTTAATTGATGCAAGTTTAAATTCAGAAATATTTC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.3%; Score 155; DB 13; Length 4465; 100.0%; Pred. No. 2.1e-22; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Expression-type plasmid pBMSP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3613 AATAACTGATTATATCAGCTGGTACATTGCCGTAG 3579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 AATAACTGATTATATCAGCTGGTACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified_base; LOCATION: (2214)..(2215); OTHER INFORMATION: a, c, t or g US-10-047-542-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (2150) TOTHER INFORMATION: a, c, t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-10-047-542-100/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
```

```
Sequence 101, Application US/10047542
; Sequence 101, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
   APPLICANT: INFORMATION:
   APPLICANT: WYCOFF, KEITH L.
   TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
   TITLE OF INVENTION: NOVEL IMMUNERSES
; FILE REFERENCE: 030905.0004.CIP1
   CURRENT FILING DATE: 2001-10-26
; FRIOR APPLICATION NUMBER: E0/20
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SEQ ID NO 101
; SEQ ID NO 111
                                                                                                                                                                                                                                                                                                                                                                  5811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      5810 TATTATAGICCAAGCAAAAAAATTATTGATGCAAGTTTAAATTCAGAAATATTC 5751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 TATTATAGTCCAAGGAAAAGATATATTGATGCAAGTTTAAATTCAGAAATATTTC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 793 TATTATAGTCCAAGCAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTC 852
                                                                                                                                                                                                                                                                                                                                                                                                                 321 TATTATAGTCCAAGCAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTC 380
                                                                                                                                                                                                                                                                                                                                                               5870 TIAATICCCATCTIGAAAGAATATAGTITAAATATITATIGATAAAATAACAAGTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 TIAATICCCATCTIGAAAGAAATATAGITTAAATATTTATTGATAAAATAACAAGTCAGG
                                                                                                                                                                                                                                                                                                                261 TTAATTCCCATCTTGAAAGAAATATAGTTTAAATATTTTATTGATAAAATAACAAGTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.3%; Score 155; DB 13; Length 7129; Best Local Similarity 100.0%; Pred. No. 2.4e-22; Matches 155; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                 Length 6602;
                                                                                                                                                                                                                 Query Match 37.3%; Score 155; DB 13; Length 6
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 155; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CRGNISM: Unknown Organism
FEATURE:
OTHER INFORMATION: DESCRIPTION Of Unknown Organism:
OTHER INFORMATION: pGPTV-hpt-ocs-35SJ/SC
US-10-047-542-101
                                                                                                                   Description of Unknown Organism:
pGPTV-kan-ocs-ATR-IgA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5750 AATAACTGATTATATCAGCTGGTACATTGCCGTAG 5716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 AATAACTGATTATATCAGCTGGTACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 AATAACTGATTATATCAGCTGGTACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATAACTGATTATATCAGCTGGTACATTGCCGTAG 887
                                            TYPE: DNA
ORGANISM: Unknown Organism
                                                                                           FEATURE:
COTHER INFORMATION:
COTHER INFORMATION:
US-10-047-542-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-10-047-542-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-10-047-542-14
SEQ ID NO 100
LENGTH: 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

; Seguence 14, Application US/10047542

```
6554 TATTATAGTCCAAGCAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTT 6613
                                                                                               6614 AATAACTGATTATATCAGCTGGTACATTGCCGTAG 6648
                                               381 ANTARCTGATTATATCAGCTGGTACATTGCCGTAG 415
                                                                                                                                                                         Search completed: December 5, 2004, 09:36:21 Job time : 331.103 secs
셤
                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09847057

Patent No. US20020004943A1

GENERAL INFORMATION:

TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLAN
FILE REPERENCE: PAGODA

CURRENT APPLICATION NUMBER: US/09/847,057

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0
          FUDITICATION NO. USZUGZIOSBS/AIL

APPLICANT: LARRICK, JAMES W.

APPLICANT: LARRICK, JAMES W.

APPLICANT: WAYCOFF, KEITH L.

ITILE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

ITILE OF INVENTION: AND BACTERIAL DISEASES

FILE REFERENCE: 030905.0004.CIP1

CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-04-28

PRIOR APPLICATION NUMBER: 60/200,298

PRIOR PILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SEQ ID NO 14

LENGTH: 8074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6494 TIAATICCCATCTIGAAAGAATATAGTITAAATATTTATIGATAAAATAACAAGICAGG 6553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 TATTATAGTCCAAGCAAAAAGTTAATGATGCAAGTTTAAATTCAGAAATATTC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 TATTATAGTCCAAGCAAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         793 TATTATAGTCCAAGCAAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTC 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.3%; Score 155; DB 13; Length 8074; Best Local Similarity 100.0%; Pred. No. 2.5e-22; Matches 155; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
37.3%; Score 155; DB 9; Length 8340;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 155; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Expression-type plasmid pBMSP-1spJSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 AATAACTGATTATATCAGCTGGTACATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAACTGATTATATCAGCTGGTACATTGCCGTAG 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Binary vector pAGI4002
US-09-847-057-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

NAME/KEY: modified_base

COCATION: (2315)

CTHER INFORMATION: a, c, t or g
US-10-047-542-14
Publication No. US20020168367A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-847-057-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```